

Delaval, Jan

75185 .

From: Huynh, Phuong N.
Sent: Monday, September 09, 2002 1:11 PM
To: Delaval, Jan
Subject: RE: 09/811,367

Jan,

Please search polypeptide of SEQ ID NO: 1 against commercial and interference databases.

Thanks,
Neon
Art unit 1644
Mail 9E12
Tel 308-4844

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
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OM protein - protein search, using sw model

Run on: September 9, 2002, 14:54:46 ; Search time 16.41 Seconds
(without alignments)
1106.696 Million cell updates/sec

Title: US-09-811-367B-1

Perfect score: 1023

Sequence: 1 MTDVSIYSMLPEPTAQACN.....GLQASCEVPLHGVCCKVRL 189

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	525.5	51.4	188	159421	mast cell function
2	201	19.6	225	138700	hNKR-p1a protein -
3	193	18.9	257	150146	gene 17.5 protein -
4	191	18.7	227	A46467	natural killer cel
5	190	18.6	233	PT0372	natural killer cel
6	182	17.8	231	PT0374	natural killer cel
7	180	17.6	216	PT0375	natural killer cel
8	178.5	17.4	240	154524	natural killer cel
9	176	17.2	404	A46274	HLV gp120-binding
10	175.5	17.2	223	A35917	NK-cell receptor p
11	174.5	17.1	304	JX0209	lectin, galactose/
12	174	17.0	139	JH0822	lymphocyte early a
13	169	16.5	237	UC7608	type II lectin-like
14	167	16.3	301	S13165	asialoglycoprotein
15	166	16.2	156	T28141	C type lectin, B1
16	165	16.1	284	S29855	asialoglycoprotein
17	164.5	16.1	306	A42230	lectin M-ASGP-BP p
18	162	15.8	262	A30573	T-cell surface gly
19	162	15.8	262	A45813	NKR-p1 protein hom
20	160.5	15.7	223	B46467	hepatic lectin 2 -
21	160.5	15.7	284	1LNRTL	hepatic lectin 2 -
22	160.5	15.7	301	1LNRTL	hepatic lectin 2 -
23	157.5	15.4	291	1LNHT1	hepatic lectin H1
24	157	15.3	262	I49361	natural killer cel
25	156	15.2	1487	A48719	phospholipase-A(2)
26	153.5	15.0	167	1WMVF2	hepatic lectin hom
27	151.5	14.8	260	2I49049	Ly-49D-GE antigen
28	149	14.6	170	2T8140	natural killer cel
29	148.5	14.5	220	C46467	NKR-p1 protein hom

30	148.5	14.5	550	2	A28166	Kupffer cell recep
31	146.5	14.3	1326	2	B56395	secretory phosphol
32	146.5	14.3	1465	2	A56395	secretory phosphol
33	146	14.3	311	1	LNH02A	asialoglycoprotein
34	145.5	14.2	1479	2	T42710	mannose receptor,
35	143.5	14.0	144	2	PC7027	aggrelin alpha cha
36	142	13.9	146	2	JC7135	agglutinin beta
37	141.5	13.8	1458	1	A49707	phospholipase A2 r
38	140.5	13.7	267	2	I49053	Ly-49G.2 antigen
39	140.5	13.7	280	2	I49052	Ly-49G.1 antigen
40	139.5	13.6	3562	2	A47171	chondroitin sulfat
41	138.5	13.5	1463	2	A53210	pancreatic stone p
42	137.5	13.4	175	2	S29822	pancreatic stone p
43	137	13.4	165	2	A28351	pancreatic stone p
44	137	13.4	266	2	I49363	natural killer cel
45	137	13.4	742	2	JC7595	scavenger receptor

ALIGNMENTS

RESULT 1
159421
mast cell function associated antigen - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
R:Guthmann, M.D.; Tal, M.; Pecht, I.
Proc. Natl. Acad. Sci. U.S.A. 92, 9397-9401, 1995
A:Title: A secretion inhibitory signal transduction molecule on mast cells is another
A:Reference number: 159421; MUID:96016176
A:Accession: 159421
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-188 <RES>
A:Cross-references: EMBL:X79812; NID:g1020141; PIDN:CA56208.1; PID:g1020142
A:Gene: mafa

Query Match 51.4%; Score 525.5; DB 2; Length 188;

Best Local Similarity 53.5%; Pred. No. 4.6e-42;

Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;

QY 1 MTDVSIYSMLPEPTAQACNDYGPQOKSSSKPSCCLVAITLGLTAVLLSYLVYOWIL 60
DB 1 MADNSITSTLELPAPRVQDDSRWKYKAVLHRCVSYLVWVALLGLTILMSLLYORTL 60
QY 61 CGSNSTICASCPCPDNRWKYGNHCYFVSVEKDMNSLFECLARDSHLVTDOEMS 120
DB 61 CCGSGFMCSCRCPPNLMRMNGSHCYFSMEKRDWNSSLKFCADKSHLTFPPDQVVA 120
QY 121 LLOVRLSEAFICWIGIRNNSGWRMGEDGSPILNFSRISNSNVQPCGALNKNGLQASCEVPL 180
DB 121 LFQEVGEDFTWIGRLDIDGWRMGEDGSPALISLILSNVYQKCGTIRGHLASCEVAL 179
QY 181 HGVCCKV 187
DB 180 QWICEKV 186

RESULT 2

138700
hNKR-p1a protein - human
C:Species: Homo sapiens (man)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
C:Accession: 138700
R:Lanier, L.L.; Chang, C.; Phillips, J.H.
J. Immunol. 153, 2417-2428, 1994
A:Title: Human NKR-p1a: A disulfide-linked homodimer of the C-type lectin superfamily
A:Reference number: 138700; MUID:943554407
A:Accession: 138700
A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA
 A:Residues: 1-225 <RES>
 A:Cross-references: EMBL:U11276; NID:9538270; PIDN:AAA21605.1; PID:9544496
 C:Superfamily: natural killer cell receptor PI, C-type lectin homology
 F:94-210/Domain: C-type lectin homology <LCH>

Query Match 19.6%; Score 201; DB 2; Length 225;
 Best Local Similarity 26.0%; Pred. No. 1.7e-11;
 Matches 58; Conservative 36; Mismatches 81; Indels 48; Gaps 8;

1 MNDVSYSMLTPTAQAQNDVGPQKSSSSK-----SCSCLVATITG 44
 1 MDQAIVAEILNLP-----DSGPSSPSLPDVCQSPHOFALKSCAGITILLVL- 53
 45 LTLAVLLSVLLXOMILCOGSNSTCA-----SCSPCDPMKMYGNHCYFYS 90
 54 VVTGLSVST-----SLIOKSSIEKCSVDIQSNKKTPTERPGLNCPYWGQLREKCLIFS 109
 91 VEKDMNSLEFLARDSHLVITDQEMSLVFLSE--AFCWIGLR--NNSGWRMED 145
 110 HVTNPNNSLADSTKESLLIRDEDLHTQNLIRDKAILFWIGLNFSLSEKMKWIN 169
 146 GSPINFS--RISNSFVOTCGAINKNGLOASCEVPLHGVCCK 186
 170 GSTLNSNDIEIRDAKENSICISQTSVISEYCTEIRMICOK 212

RESULT 3
 150146
 gene 17.5 protein - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
 C:Accession: 150146
 R:Bernot, A.; Zoorob, R.; Auffray, C.
 Immunogenetics 39, 221-229, 1994
 A:Title: Linkage of a new member of the lectin supergene family to the chicken Mhc genes
 A:Reference number: 150146; MVID:9416461
 A:Accession: 150146
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-257 <BER>
 A:Cross-references: GB:M88072; NID:9505324; PIDN:AAA8556.1; PID:9505325
 C:Superfamily: C-type lectin homology
 F:123-241/Domain: C-type lectin homology <LCH>

Query Match 18.9%; Score 193; DB 2; Length 257;
 Best Local Similarity 26.6%; Pred. No. 1.1e-10;
 Matches 49; Conservative 28; Mismatches 89; Indels 18; Gaps 4;

17 QAQNDYGPQKSSSSKSCSCL-----VAITGLTAVLLSVLLXOMILCOGSNSTC 69
 64 EATTRGDEBERGQSGSELRNRRVYLVALSAVPCULVALAVIYLGRPS---C 119
 70 ASCPS---CPDRMKYGNHCYFYSVEKDMNSLEFLARDSHLVITDQEMSLQVF 125
 120 SRPPEHVCNPAWVGFOGCVYSDTESDMNSRCHRLGSLATLIDKEEPEFLQY 179
 126 LSEAFWICGRNNSG---NRMEDGSPINFSRISNSFVOTCGAINKNGLOASCEVPLHG 182
 180 QNRADWIGLHRAEGDEHWTADGSAFTNRPVELKGGCAVLNGDGISALCHSEKFW 239
 183 VCKK 186
 240 VCSR 243

RESULT 4
 A46467
 natural killer cell receptor PI - mouse
 N:Alternate names: NKR-PI protein
 C:Species: Mus musculus (house mouse)

C:Date: 18-Jun-1993 #sequence_revision 19-Feb-1999 #text_change 05-May-2000
 C:Accession: A46467; A46502; A46456
 R:Giorda, R.; Trucco, M.
 J. Immunol. 147, 1701-1708, 1991
 A:Title: A family of genes selectively coexpressed in adherent lymphokine-activated K
 A:Reference number: A46467; MVID:91349596
 A:Accession: A46467

A:Molecule type: mRNA
 A:Residues: 1-227 <GIO>
 A:Cross-references: GB:M7676; NID:9200058
 A:Experimental source: A-TAK cells, C57BL
 A:Note: sequence extracted from NCBI backbone (NCBIN:52378, NCBIPI:52379); the sequenc
 R:Giorda, R.; Welsberg, E.P.; Ip, T.K.; Trucco, M.
 J. Immunol. 149, 1957-1963, 1992
 A:Title: Genomic structure and strain-specific expression of the natural killer cell
 A:Reference number: A46502; MVID:92388663
 A:Accession: A46502

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-109, 'H', 111-181, 'D', 183-227 <GI2>
 A:Cross-references: GB:X64716; NID:933393; PIDN:CAA45971.1; PID:9817989
 A:Experimental source: BALB/c 3T3 fibroblastoid cell line
 A:Note: sequence extracted from NCBI backbone (NCBIN:113037, NCBIN:113063, NCBIN:1130
 J:Yokoyama, W.M.; Ryan, J.C.; Hunter, J.J.; Smith, H.R.; Stark, M.; Seaman, W.E.
 J. Immunol. 147, 3229-3236, 1991

A:Title: CDNA cloning of mouse NKR-PI and genetic linkage with Lx-49. Identification
 A:Reference number: A46456; MVID:92013158
 A:Accession: A46456

A:Molecule type: mRNA
 A:Residues: 1-38, 'L', 40-227 <YOK>
 A:Cross-references: GB:M7753; NID:9198569; PIDN:AAA9366.1; PID:9198570

A:Note: sequence extracted from NCBI backbone (NCBIN:60429, NCBIPI:60431)
 C:Superfamily: natural killer cell receptor PI, C-type lectin homology
 F:94-210/Domain: C-type lectin homology <LCH>

Query Match 18.7%; Score 191; DB 2; Length 227;
 Best Local Similarity 27.4%; Pred. No. 1.5e-10;
 Matches 49; Conservative 43; Mismatches 71; Indels 16; Gaps 7;

24 POKSSSSKSCSCLVATITGLT-TAVLLSVLLXQ-----WILCOGS-NYST-CASCPS 74
 34 PRHSRSLKLSLSCAGLILVYTLIGMSVLYRLQKPSIEKCYVLIQENLNTTDCSAKLE 93
 75 CPDRMKYGNHCYFYSVEKDMNSLEFLARDSHLVITDQEMSLQVFLSAP--CW 132
 94 CPQDWLSHRDKCFHVSQVSTWEGLVDCDGGKATMLIDQOEBLRFLLDSIKERKYNFSW 153
 133 IGUR---NNSGWRMEDSPINFS--RISNSFVOTCGAINKNGLOASCEVPLHGVCCK 186
 154 IGLRYTLPLDPMKMKWINGSTLNSDVLKITGTENDSCAISQDKVTFESCSNDNRMICOK 212

RESULT 5
 P70372
 natural killer cell receptor group 2, splice form A - human

N:Alternate names: NKG2-A; NKG2-B
 N:Containing: natural killer cell receptor group 2, splice form B
 C:Species: Homo sapiens (man)
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 05-May-2000
 C:Accession: P70372; MVID:91178434
 R:Houchins, J.P.; Yabe, T.; McSherry, C.; Bach, F.H.
 J. Exp. Med. 173, 1017-1020, 1991
 A:Title: DNA sequence analysis of NKG2, a family of related CDNA clones encoding type
 A:Reference number: P70372; MVID:91178434
 A:Accession: P70372

A:Molecule type: mRNA
 A:Residues: 1-233 <HOUI>
 A:Cross-references: EMBL:X54867; NID:935056; PIDN:CAA38649.1; PID:935057
 A:Experimental source: natural killer cell
 A:Accession: P70373
 A:Molecule type: mRNA
 A:Residues: 1-95, 114-233 <HOUI2>

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A:Cross-references: GB:X54868; NID:g35058; PIDN:CAA8650.1; PID:g35059
A:Experimental source: natural killer cell
C:Genetics:
A:Gene: GDB:KLRCL; NKG2
A:Cross-references: GDB:138773; OMIM:161555
A:Map position: 12pter-12qter
C:Superfamily: natural killer cell receptor PL; C-type lectin homology
C:Keywords: alternative splicing; glycoprotein; transmembrane protein
F:119-229/Domain: transmembrane #status predicted <TRA>
F:102,103,151,180/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:119-130,147-229,208-221/Disulfide bonds: #status predicted

Query Match 18.6%; Score 190; DB 2; Length 233;
Best Local Similarity 27.8%; Pred. No. 1.9e-10;
Matches 55; Conservative 35; Mismatches 86; Indels 22; Gaps 8;

OY 5 VIYSMLPFAQNDNYGPOOKSSSK--PSC-SCVAITGLTAVLL----SVLYQ 57
DB 38 IYYAELNLQKASQ---DFQNDKRYHCKDLPAPKELVIGILIGITLIIMASVYTIYIP 94
OY 58 WILCGSNST-----CASCPCPDPMKMYGNHCYFFSVEEKDNSSLFCLARDSHL 110
DB 95 STLIOHNNSSLMTRTQOKARHCCHCPPEMITYSNCCYFGKRRRTWEESILACTSKNSL 154
OY 111 LVITDDEMSLTVFUSEAFQWIGL--RNSGMRWEDSGPLNSR--ISSNSFVOTGAIN 167
DB 155 LSIDNEEKFLSIISPS--WIGVFRNSHHPWTVMGLAFKHEIKDSDNALNCVILQ 212
OY 168 KNLQASGCEVPLHGVCK 185
DB 213 VNLKSAOCSSIIYHCK 230

RESULT 6
PT0374
natural killer cell receptor group 2-C, splice form 1 - human
N:Alternate names: NKG-C
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1992 #sequence, revision 31-Mar-1992 #text_change 19-May-2000
C:Accession: PT0374
R:Houchins, J.P.; Yabe, T.; McSherry, C.; Bach, F.H.
J. Exp. Med. 173, 1017-1020, 1991
A:Title: DNA sequence analysis of NKG2, a family of related cDNA clones encoding type II
A:Reference number: PT0372; MVID:91178434
A:Accession: PT0374
A:Molecule type: mRNA
A:Residues: 1-231 <HOU>
A:Cross-references: EMBL:X54869; NID:g35060; PIDN:CAA38651.1; PID:g35061
A:Experimental source: natural killer cell
C:Genetics:
A:Gene: GDB:KLRG2; NKG2-C
A:Cross-references: GDB:9787095
A:Map position: 12p13-12p13
C:Superfamily: natural killer cell receptor PL; C-type lectin homology
C:Keywords: glycoprotein; transmembrane protein
F:71-96/Domain: transmembrane #status predicted <TRA>
F:27,100,149,178/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 17.8%; Score 182; DB 2; Length 231;
Best Local Similarity 27.8%; Pred. No. 1.1e-09;
Matches 47; Conservative 32; Mismatches 76; Indels 14; Gaps 5;

OY 24 POKSSSKPSCGLVAITGLTAVLLSVLLYQWILCOGSNST*---CASCPCPDRAW 79
DB 67 PEKPLAEVIGIICIV-----LMAFVLTIVLIFLEONSSPNRTOKARHCCHPEEW 121
OY 80 KMYGNHCYFVSVEEKDNSSLFCLARDSHLTVITDDEMSLLOVFLSAPFCWIGL--RNN 138
DB 122 IYNSNCYIIGKRRRTWEESILACTSKNSLISIDNEEIKFLASILPS--WIGVFRNS 179

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Oy 139 SCWRHEDSPINLEFSR--ISSNSFVOTGCAIKKNGLOASSCEVPLHGVC 185
 Db 180 SHHPWVTINGLAIFKHKIKDSDAELNCAVLQYNRLKSAQCGSSMYTHCK 228
 RESULT 7
 PT0375
 natural killer cell receptor group 2-D - human
 N:Alternate names: Integral membrane protein NKG2-D
 C:Species: Homo sapiens (man)
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 05-May-2000
 C:Accession: PT0375; S15671; S19110
 R:Houchins, J.P.; Yabe, T.; McSherry, C.; Bach, F.H.
 J. Exp. Med. 173, 1017-1020, 1991
 A:Title: DNA sequence analysis of NKG2, a family of related cDNA clones encoding type
 A:Reference number: PT0372; MUID:91178434
 A:Accession: PT0375
 A:Molecule type: mRNA
 A:Residues: 1-126 <HOU>
 A:Cross-references: EMBL:X54870; NID:g935062; PIDD:CA38652.1; PID:g935063
 A:Experimental source: natural killer cell
 A:Note: translation of nucleotide sequence is not complete
 C:Keywords: transmembrane protein

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Query March          17.6% Score 180; DB 2; Length 216;
Best Local Similarity 26.8%; Pred. No. 1.5e-09;
Matches 42; Conservative 31; Mismatches 52; Indels 32; Gaps 5;

QY   37 CLVAITLG-----LTLAVLLSVLYQMILCOGSNYSTCASCPSPDRMKYNHCYR 88
      ||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db    57 CFIAVMGIRFLIMAWIASVAFNSLFNQEVQIP----LFTSYCGPCPKMICYKNNCYO 112

QY   89 FSEVEKMNSSLFCLARDSHLVITTDNQEMLQLQVLSEAPFCWIGL---RNNGWRRED 145
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db    113 FFDESKMYTESQASCMSONASLKYTSKEPDLLK--LKYSYHMGGLVIHIPTPNSQMOWED 170

QY   146 GSPLNFSTR-----SSNSEFYOTGCAGIN 167
      ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db    171 GSILSPNLITTIEMOKGDCALAYASFPGIYINCSTPN 207

RESULT      8
154524
natural killer cell receptor group 2-C, splice form 2 - human
C:Species: Homo sapiens (man)
C>Date: 07-Jun-1996 #sequence-revision 07-Jun-1996 #text-change 19-May-2000
C:Accession: I54524
R:AAdamkiewicz, T.V.; McSherry, C.; Bach, F.H.; Houchins, J.P.
ImmunoGenetics 39, 218, 1994
A>Title: Natural killer lectin-like receptors have divergent carboxy-termi., distance
A:Reference number: I54524; MWID:P4102823

A:Accession: I54524
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-240 <RES>
A:Cross-references: GB:IJL4542; NID:g292360; PIDD:NAA1833.1; PID:g292361
C:Genetics:
A:Gene: GDB:KLRC2; MKG2-C
A:Cross-references: GDB:9787095
A:Map position: 12p13-12p13
C:Superfamily: natural killer cell receptor P1; C-type lectin homology

Query Match          17.4% Score 178.5; DB 2; Length 240;
Best Local Similarity 28.6%; Pred. No. 2.4e-09;
Matches 46; Conservative 30; Mismatches 70; Indels 15; Gaps 6;

QY   24 POCKSSSRPSCSCLVAITLGLTFAVLISVLYQMILCOGSNST-----CASCPSPDRW 79
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db    67 PPRLTRLEVALICIV-----LMATVLTAKTVLPFLPONNSSPPTRFKARPCGHCEPEW 121

QY   80 MKYGNHCYFSVEEKDNSSLFCLARDSHLVTDD-NQEMLQLQVLSEAPFCWIGL-RN 137

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Db 122 ITYSNCTYIKERTWEESLOACASKNSSSLIDNEEMFLSLIPSS--WIGVFEN 179
 QY 138 NSGWMEDGSPINFSR--ISSNSFYOTCGAINKNGLOASSC 176
 Db 180 SSHHPWVTINGLAFFKEIKSDHAERNCAMLHVRLISDQC 220

RESULT 9
 A46274
 HIV gp120-binding C-type lectin - human
 C:Species: Homo sapiens (man)
 C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 01-Dec-1995
 C:Accession: A46274
 R:Curtis, B.M.; Scharnowski, S.; Watson, A.J.
 Proc. Natl. Acad. Sci. U.S.A. 89, 8356-8360, 1992
 A:Title: Sequence and expression of a membrane-associated C-type lectin that exhibits CD
 A:Reference number: A46274; MUID:92390446
 A:Accession: A46274
 A:Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-404 <CDR>
 A:Experimental source: placenta
 A:Note: sequence extracted from NCBI backbone (NCBIN:113134, NCBIPI:113135)
 F:256-377/Domain: C-type lectin homology <LCH>

Query Match 17.2%; Score 176; DB 2; Length 404;
 Best Local Similarity 30.7%; Pred. No. 6,9e-09;
 Matches 39; Conservative 23; Mismatches 53; Indels 12; Gaps 5;

QY 72 CPSCDPRMKYGNHCYFVSVEEKDNSSLEFCLARDSHLVTIDNQMSLQVFLSEA-- 129
 Db 253 CHPEPWETTFQOCNYCFMNSQRMHDSITACKVEGAQLVIKSAEQNFLQSSRSNR 312
 QY 130 FCWIGLR--NNSG-WRMEDGSP--NFSRI-----SSNSFYOTCGAINKNGLOASSCEVP 179
 Db 313 FFWMLSPDNQBGITQWQVDSPLPSPFOYNNRGNPNNGEEDCAEFSSGNNNDKCNDA 372

QY 180 LHGVCK 186
 Db 373 KFWICK 379

RESULT 10
 A35917
 NK-cell receptor P1 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 24-Sep-1999
 C:Accession: A35917
 R:Giordano, R.; Rudeart, W.A.; Vavassori, C.; Chambers, W.H.; Hiserodt, J.C.; Trucco, M.
 Science 249, 1298-1300, 1990
 A:Title: NKR-P1, a signal transduction molecule on natural killer cells.
 A:Reference number: A35917; MUID:90378305
 A:Accession: A35917
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-223 <GIO>
 A:Cross-references: GB:M62891; NID:g205722; PIDN:AAA41710.1; PID:g205723
 C:Superfamily: natural killer cell receptor P1; C-type lectin homology
 C:Keywords: transmembrane protein
 F:94-210/Domain: C-type lectin homology <LCH>

Query Match 17.2%; Score 175.5; DB 2; Length 223;
 Best Local Similarity 27.1%; Pred. No. 4.2e-09;
 Matches 49; Conservative 44; Mismatches 67; Indels 21; Gaps 9;

QY 24 PQQKSSSKPSCSCLVATLGLT-TAVLLSVLYO-----WILCOGSNYSTCASCPS-- 74
 Db 35 PRSHLALKLSGAGLILVALVGSILVRYVQKPSVPCRVLIQ-ENLSKTGS-PAKL 92

QY 75 -CPDRMKYGNHCYFVSVEEKDNSSLEFCLARDSHLVTIDNQMSLQVFLSEA-- 130
 Db 93 KCPKDWLSHRDCFHVSOFTSTWESLADCGGAGATLLVQDDELFNLTKRISSSF 152
 QY 131 CWIGLR--NNSGWMEDGSPINF--RISNSFYOTCGAINKNGLOASSCEVP 185
 Db 153 -WIGLSYTLSDENMKWKINSTLNSDVLSTIGDEKSCASVSQDKVLSQSCSDNINWQC 211

QY 186 K 186
 Db 212 K 212

RESULT 11
 JX0209
 lectin, galactose/N-acetylglucosamine-specific - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Aug-1999
 C:Accession: JX0209; PX0009
 R:Sato, M.; Kawakami, K.; Osawa, T.; Toyoshima, S.
 J. Biochem. 111, 331-336, 1992
 A:Title: Molecular cloning and expression of cDNA encoding a galactose/N-acetylglact
 A:Reference number: JX0209; MUID:92268032
 A:Accession: JX0209
 A:Molecule type: mRNA
 A:Residues: 1-304 <SAT>
 A:Cross-references: GB:S36676; NID:g249360; PIDN:AAB22171.1; PID:g249361
 R:Oda, S.; Sato, M.; Toyoshima, S.; Osawa, T.
 J. Biochem. 104, 600-605, 1988
 A:Title: Purification and characterization of a lectin-like molecule specific for gal
 A:Reference number: PX0009; MUID:89197865
 A:Accession: PX0009
 A:Molecule type: Protein
 A:Residues: 102-120;137,'X',139-151 <ODA>
 C:Superfamily: hepatic lectin; C-type lectin homology
 C:Keywords: glycoprotein; lectin; macrophage; transmembrane protein
 F:35-61/Domain: transmembrane #status predicted <TRA>
 F:173-296/Domain: C-type lectin homology <LCH>
 F:74,166/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 17.1%; Score 174.5; DB 2; Length 304;
 Best Local Similarity 27.5%; Pred. No. 7.1e-09;
 Matches 39; Conservative 27; Mismatches 61; Indels 15; Gaps 5;

QY 59 ILCOGSNYSTCAS-CPSCDPRMKYGNHCYFVSVEEKDNSSLEFCLARDSHLVTIDNQ 117
 Db 156 LTCQLANLKNNGSEVACCPFLHWTEHSGCYWFSESEKSWPEADKCYRLNLSHLVNVSL 215
 QY 118 EMSLQVFLSEAFWCWIGLRNNSG-WRMEDGSP--NFSRISSNSFY-----QTCG 164
 Db 216 EONFLQNLRLANVYVSWGLTDQNGPMRWVDGTDFEKGFKWAPLQDPNWFGLGGEDECA 275
 QY 165 AINKNG-LOASSCEVP 185
 Db 276 HITGGPMNDVQCQRTFRWICE 297

RESULT 12
 JH0822
 lymphocyte early activation antigen AIM/CD69 - human
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 08-Oct-1999
 C:Accession: JH0822; I56167; S60753
 R:Lopez-Cabrera, M.; Santis, A.G.; Fernandez-Ruiz, E.; Blacher, R.; Esch, F.; Sanchez
 J. Exp. Med. 178, 537-547, 1993
 A:Title: Molecular cloning, expression, and chromosomal localization of the human ear
 A:Reference number: JH0822; MUID:93340630
 A:Accession: JH0822
 A:Molecule type: mRNA
 A:Residues: 1-199 <LOP>
 A:Cross-references: GB:222576; NID:g397938; PIDN:CAA80298.1; PID:g397939

A>Note: the authors translated the codon CAA for residue 110 as Glu
 R:Hamann, J.; Fiebig, H.; Strauss, M.
 J. Immunol. 150, 4920-4927, 1993
 A:Title: Expression cloning of the early activation antigen CD69, a type II integral mem
 A:Accession number: 156167; MUID:93267093
 A:Accession: 156167
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-199 <S>
 A:Cross-references: GB:L07555; NID:g291897; PIDN:AB46359.1; PID:g291898
 R:Sanlits, A.G.; Lopez-Cabrea, M.; Hamann, J.; Strauss, M.; Sanchez-Madrid, F.
 Eur. J. Immunol. 24, 1692-1697, 1994
 A:Title: Structure of the gene coding for the human early lymphocyte activation antigen
 ceptors.
 A:Reference number: S60753; MUID:94298875
 A:Accession: S60753
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-199 <S>
 A:Cross-references: EMBL:Z30426; NID:g525242; PIDN:CAA83017.1; PID:g558352
 C:Comment: This protein is the earliest inducible cell surface glycoprotein expressed in
 C:Genetics:
 A:Gene: GDB:CD69
 A:Cross-references: GDB:132925; OMIM:107273
 A:Map position: 12p13-12p12
 C:Superfamily: C-type lectin homology
 C:Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein
 F:38-64/Domain: transmembrane #status predicted <TM>
 F:85-194/Domain: C-type lectin homology <LCH>
 F:18,30/Binding site: phosphate (ser) (covalent) (by protein kinase C) #status predicted
 F:31/Binding site: phosphate (thr) (covalent) (by casein kinase II) #status predicted
 F:166/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 17.0%; Score 174; DB 2; Length 199;
 Best Local Similarity 22.9%; Pred. No. 5.2e-09;
 Matches 40; Conservative 33; Mismatches 76; Indels 26; Gaps 5;

QY 30 SSRKSCIVAITGLTAVLLSVLYLWILCOGSSNYSTCASC-----SC 75
 DB 30 STRHSGFOYVPLCAVMNVPTITLILALISVGQY---NCPQYTFSPMSDSHVSQC 85
 QY 76 PDRMKAGNHCYFSEVEKDNNSLEFCLARDSHLVITDQEMSLQVFLSEAFQWIGL 135
 DB 86 SEDVVGQKRCYFTSVKRSSTSAONACSEHGATLAVIDSEKDMFLKRYAREEHVWGL 145
 QY 136 RNSG--WRWEDGSPLN--FSRISNSFEVOTCGAINKGLQASSCEVPLHGVCKR 186
 DB 146 KKEGHPMKWMSNGKEFNMFVVTGSDK---CVFLKTEVSSMECEKNLYWICNK 196

RESULT 13
 JC7608
 Type II lectin-like immunoreceptor - human
 C:Species: Homo sapiens (man)
 C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
 C:Accession: JC7608
 R:Hamann, J.; Fiebig, H.; Strauss, M.; Hamann, J.; Strauss, M.; Sanchez-Madrid, F.
 Eur. J. Immunol. 24, 1692-1697, 1994
 A:Title: Expression cloning of the early activation antigen CD69, a type II integral mem
 A:Accession number: 156167; MUID:93267093
 A:Accession: 156167
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-199 <S>
 A:Cross-references: GB:L07555; NID:g291897; PIDN:AB46359.1; PID:g291898
 R:Sanlits, A.G.; Lopez-Cabrea, M.; Hamann, J.; Strauss, M.; Sanchez-Madrid, F.
 Eur. J. Immunol. 24, 1692-1697, 1994
 A:Title: Structure of the gene coding for the human early lymphocyte activation antigen
 ceptors.
 A:Reference number: S60753; MUID:94298875
 A:Accession: S60753
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-199 <S>
 A:Cross-references: EMBL:Z30426; NID:g525242; PIDN:CAA83017.1; PID:g558352
 C:Comment: This protein is the earliest inducible cell surface glycoprotein expressed in
 C:Genetics:
 A:Gene: GDB:CD69
 A:Cross-references: GDB:132925; OMIM:107273
 A:Map position: 12p13-12p12
 C:Superfamily: C-type lectin homology
 C:Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein
 F:38-64/Domain: transmembrane #status predicted <TM>
 F:85-194/Domain: C-type lectin homology <LCH>
 F:18,30/Binding site: phosphate (ser) (covalent) (by protein kinase C) #status predicted
 F:31/Binding site: phosphate (thr) (covalent) (by casein kinase II) #status predicted
 F:166/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 16.5%; Score 169; DB 2; Length 237;
 Best Local Similarity 21.6%; Pred. No. 1.8e-08;
 Matches 52; Conservative 39; Mismatches 92; Indels 58; Gaps 9;

QY 1 MTDVSYIMLEL-----PTAQOANDYQPOQSSSSKSPSCSLVATGLTAVL 50
 DB 1 MTESEITAAVRRKNEKSSGINTMSSAASKERAPLPSNTGFFKLKALIFELLALS 60
 QY 51 LSV-----LLYQWILCOGSSNY---STCASCPCPDPRMKYGNHCY 87
 DB 61 FPIAVYIFPOKYSOLLEKTKETKELVTTLECYKKNMPVEETAWSC--CPKRMKSFSSNCY 118
 QY 88 YPSVEKDNNSLEFCLARDSHLVITDQEMSLQVFLSEAFQWIGLRLNNSG---WRW 143
 DB 119 FISTASAKQDEKDCARNAHLVINTQEBDFITQNLQESAIYVGLSDPEGQRHWR 178
 QY 144 EDGSPLEFSRISNSP-----VQTGAIN-----KNGLOASSCEVPLHGVCKR 188
 DB 179 VQQTFFYN---ESSFTFHPREPSDPRNERCVLNFRRKSPKRMGNVNCIGPORSVCEMMK 234
 QY 189 L 189
 DB 235 I 235

RESULT 14
 S13165
 Asialoglycoprotein receptor - mouse
 N:Alternate names: hepatic lectin
 C:Species: Mus musculus (house mouse)
 C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Aug-1999
 C:Accession: S13165
 R:Sanford, J.P.; Doyle, D.
 Biochim. Biophys. Acta 1087, 259-261, 1990
 A:Title: Mouse asialoglycoprotein receptor cDNA sequence: conservation of receptor ge
 A:Reference number: S13165; MUID:91027942
 A:Accession: S13165
 A:Molecule type: mRNA
 A:Residues: 1-301 <S>
 A:Cross-references: EMBL:X53042; NID:g53104; PIDN:CAA37211.1; PID:g53105
 C:Superfamily: hepatic lectin; C-type lectin homology
 C:Keywords: glycoprotein; liver; transmembrane protein
 F:170-293/Domain: C-type lectin homology <LCH>

Query Match 16.3%; Score 167; DB 2; Length 301;
 Best Local Similarity 25.9%; Pred. No. 3.6e-08;
 Matches 55; Conservative 29; Mismatches 72; Indels 56; Gaps 9;

QY 27 KSSSKPSCSLVAT---TLGLTAVLL-----SVLLY----- 56
 DB 92 KETFSNFSSSTLMERGALDTLGGSTNAILTSMIAOLEKQOOLKADHSTLLFLKHPMD 151
 QY 57 -QWILCO---GSNYSTCASCPCPDPRMKYGNHCYFSEVEKDNNSLEFCLARDSHLL 111
 DB 132 LRTFLCQLAIPRSGNGTEC-----CPVNWYFEGSCGWFPSRDGLTAEADQYCOLLENANHL 206
 QY 112 VITDQEMSLQVFLSEAFQWIGLRLNNSG--WRWEDGSPLEFSRISNSPVO----- 161
 DB 207 VINSREDOEFVVKHRSQFIHWIGLTDROGSMKMWVDDTQYR--SNYRMWAFQPDNMQGHQ 265
 QY 162 ---TCGAINKNG--LOASSCEVPLHGVCKR 188
 DB 266 GGEDCAETLSDGHMNDNFCQOVNRMVCEKR 297

RESULT 15
 T28141
 C type lectin, B locus - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T28141

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 9, 2002, 15:00:06 ; Search time 11.9 seconds

(without alignments)
614.958 Million cell updates/sec

Title: US-09-811-367b-1

Perfect score: 1023

Sequence: 1 MTDSEVYSMELPTATQAN.....GLQASSCVEPLHGVCCKVRL 189

Scoring table: BIOSUM62

Gapop 10.0, Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	196.5	19.2	179	1	CD94_HUMAN
2	196.5	19.2	199	1	CD69_MOUSE
3	191	18.7	227	1	NK11_MOUSE
4	190	18.6	233	1	NKGA_HUMAN
5	186	18.2	231	1	NKGC_HUMAN
6	180	17.6	216	1	NKGD_HUMAN
7	178.5	17.4	240	1	NKGE_HUMAN
8	175.5	17.2	223	1	NK13_RAT
9	174.5	17.1	304	1	MMGL_MOUSE
10	174	17.0	199	1	CD69_HUMAN
11	168	16.4	149	1	LEC1_HUMAN
12	167	16.3	301	1	LEC1_MOUSE
13	164.5	16.1	306	1	MMGL_RAT
14	163.5	16.0	283	1	LEC1_MOUSE
15	162	15.8	262	1	LY4A_MOUSE
16	160.5	15.7	223	1	NK12_MOUSE
17	160.5	15.7	283	1	LEC1_RAT
18	157.5	15.4	290	1	LEC1_HUMAN
19	156.5	15.3	163	1	V339_FOWPY
20	156.5	15.3	167	1	LEC1_RAT
21	153.5	15.0	167	1	V008_FOWPY
22	151.5	14.8	220	1	NK14_MOUSE
23	148.5	14.5	220	1	NK14_MOUSE
24	148.5	14.5	550	1	KOCR_RAT
25	147.5	14.4	175	1	PGCG_HUMAN
26	147	14.4	174	1	PAP3_MOUSE
27	146.5	14.3	548	1	KOCR_MOUSE
28	146	14.3	311	1	LEC1_HUMAN
29	141.5	13.8	1458	1	PA2R_RABIT
30	140.5	13.7	280	1	KLR7_MOUSE
31	139.5	13.6	3562	1	PGCV_CHICK
32	138.5	13.5	1463	1	PA2R_BOVIN
33	137.5	13.4	175	1	PAP1_MOUSE

ALIGNMENTS

RESULT	ID	CD94_HUMAN	STANDARD	PRT	AA
AC	Q13241				
DT	01-NOV-1997	(Rel. 35, Created)			
DT	01-NOV-1997	(Rel. 35, Last sequence update)			
DT	15-DEC-1998	(Rel. 37, Last annotation update)			
DE	Natural killer cells antigen CD94 (KPA3) (killer cell lectin-like receptor subfamily D, member 1).				
GN	KLRD1 OR CD94.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID-9606;				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Blood;				
RX	MEDLINE-96011848; PubMed-7589107;				
RA	Chang C., Rodriguez A., Carretero M., Lopez-Botet M., Phillips J.H., Lanier L.L.;				
RT	"Molecular characterization of human CD94: a type II membrane glycoprotein related to the C-type lectin superfamily.";				
RL	Eur. J. Immunol. 25:2433-2437(1995).				
CC	-1- FUNCTION: PLAYS A ROLE AS A RECEPTOR FOR THE RECOGNITION OF MHC CLASS I HLA-E MOLECULES BY NK CELLS AND SOME CYTOTOXIC T-CELLS.				
CC	-1- SUBUNIT: CAN FORM DISULFIDE-BONDED HETERODIMER WITH NKG2 FAMILY MEMBERS.				
CC	-1- SUBCELLULAR LOCATION: Type II membrane protein.				
CC	-1- TISSUE SPECIFICITY: NATURAL KILLER CELLS.				
CC	-1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.				
CC	-1- DATABASE: NAME=PROW; NOTE=CD guide CD94 entry; WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd94.htm".				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@sib-sib.ch).				
CC	EMBL: U30610; AAC50291.1; -				
CC	MIM: 602894; -				
DR	InterPro: IPR001304; lectin_c.				
DR	Pfam: PF00059; lectin_c; 1.				
DR	SMART: SM00034; CLECT; 1.				
DR	PROSITE: PS00615; C-TYPE_LECTIN_1; FALSE_NEG.				
DR	PROSITE: PS50041; C-TYPE_LECTIN_2; 1.				
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FT	DOMAIN	1	10		
FT	TRANSMEM	11	31		
FT	FT				
FT	DOMAIN	32	179		
FT	DOMAIN	98	176		
FT	DISULFID	61	72		
FT	DISULFID	89	174		

CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
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 CC
 CC EMBL: M77676; AAA38822.1; -
 CC EMBL: M77753; AAA39366.1; -
 CC MGD; MG1:107540; L555a.
 CC InterPro: IPR001304; lectin_c.
 CC Pfam: PF000059; lectin_c.1.
 CC SMART: SM00034; CLECT.1.
 CC PROSITE: PS00615; C-TYPE_LECTIN_1; FALSE_NEG.
 CC PROSITE: PS50041; C-TYPE_LECTIN_2; 1.
 CC GlycoProfile: Antigen; Transmembrane; Signal-anchor; Lectin.
 CC DOMAIN 1 42 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 43 62 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 CC (POTENTIAL).
 CC DOMAIN 63 227 EXTRACELLULAR (POTENTIAL).
 CC FT DOMAIN 93 212 C-TYPE LECTIN (LONG FORM).
 CC FT DISULFID 94 105 BY SIMILARITY.
 CC FT DISULFID 122 210 BY SIMILARITY.
 CC FT DISULFID 189 202 BY SIMILARITY.
 CC FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 169 169 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CONFLICT 39 39 S -> L (IN REF. 2).
 CC
 CC SQ SEQUENCE 227 AA; 25689 MW; 0599A2587DF0B615 CRC64;
 CC
 CC Query Match 18.7%; Score 191; DB 1; Length 227;
 CC Best Local Similarity 27.4%; Pred. No. 4.2e-11;
 CC Matches 49; Conservative 43; Mismatches 71; Indels 16; Gaps 7;
 CC
 CC QY 24 POKSSSKRSCSLVAITGL-TAVLSVLVLYO-----WILCOGS-NYST-CASCPS 74
 CC DB 34 PRHRSAKLSCGILLIVTLIGMSVLVYLQKPEIECYVLIQENLKNKTDSCAKLE 93
 CC QY 75 CPDRMKYGHCCYFSEVEKDNMSLEFCLARDSHLLVITDNOEMSLQVLESEAF--CW 132
 CC DB 94 CPQDMLSHDKCHVSOVSMTEGVLDCGKAGATMLIDODELRLLDSIKKYSFPM 153
 CC QY 133 IGLR---NNSGWRWEGSPINFE--RISNSFYQTCGAIKKNGLQASSCEVPLHGVCKR 186
 CC DB 154 IGLRYTLPMNMWKMINGSTLNSDLKITGDTENDSCAAGSDKVTFCSCSDNRMICOK 212
 CC
 CC RESULT 4
 CC NKGA_HUMAN STANDARD; PRT; 233 AA.
 CC AC P26715;
 CC DT 01-AUG-1992 (rel. 23. Created)
 CC DT 01-AUG-1992 (rel. 23, last sequence update)
 CC DT 01-MAR-2002 (rel. 41, last annotation update)
 CC DE NKGA-A/NKG2-B type II integral membrane protein (NKG2-A/B activating
 CC NK receptor).
 CC GN KLRCL OR NKG2A.
 CC OS Homo sapiens (Human).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 CC OX NCBI_TaxID=9606;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RX MEDLINE-91178434; PubMed-2007850;
 CC RA Houchins J.P., Yabe T., McSherry C., Bach F.H.;
 CC RT "DNA sequence analysis of NKG2, a family of related cDNA clones
 CC encoding type II integral membrane proteins on human natural killer
 CC cells";
 CC RL J. Exp. Med. 173:1017-1020(1991).

RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-96337916; PubMed-8753859;
 RA Plougastel B., Jones T., Trowsdale J.;
 RT "Genomic structure, chromosome location, and alternative splicing of
 RT the human NKG2A gene";
 RL Immunogenetics 44:286-291(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-98260668; PubMed-9598306;
 RA Plougastel B., Trowsdale J.;
 RT "Sequence analysis of a 62-kb region overlapping the human KLRG
 RT cluster of genes";
 RL Genomics 49:193-196(1998).
 CC -1- FUNCTION: PLAYS A ROLE AS A RECEPTOR FOR THE RECOGNITION OF MHC
 CC CLASS I HLA-E MOLECULES BY NK CELLS AND SOME CYTOTOXIC T-CELLS.
 CC -1- SUBUNIT: CAN FORM DISULFIDE-BONDED HETERODIMER WITH CD94.
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: THE NKG2-A AND -B PEPTIDES APPEAR TO BE
 CC -1- TISSUE SPECIFICITY: NATURAL KILLER CELLS.
 CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
 CC
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 CC
 CC EMBL: X54867; CAA38649.1; -
 CC EMBL: X54868; CAA38650.1; -
 CC EMBL: U54786; AAB17133.1; -
 CC EMBL: U54783; AAB17133.1; JOINED.
 CC EMBL: U54784; AAB17133.1; JOINED.
 CC EMBL: U54785; AAB17133.1; JOINED.
 CC EMBL: AF023840; AAC17488.1; -
 CC PIR: P03722; P03732.
 CC PIR: P03733; P03733.
 CC HSSP: P16581; 1ESL.
 CC MIM: 161555; -
 CC InterPro: IPR001304; lectin_c.
 CC Pfam: PF000059; lectin_c.1.
 CC SMART: SM00034; CLECT.1.
 CC PROSITE: PS00615; C-TYPE_LECTIN_1; FALSE_NEG.
 CC PROSITE: PS50041; C-TYPE_LECTIN_2; 1.
 CC Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin;
 CC Glycoprotein; Alternative splicing
 CC DOMAIN 1 70 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 71 93 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 CC (POTENTIAL).
 CC DOMAIN 94 233 EXTRACELLULAR (POTENTIAL).
 CC FT DOMAIN 118 231 C-TYPE LECTIN (LONG FORM).
 CC FT DISULFID 119 130 BY SIMILARITY.
 CC FT DISULFID 147 229 BY SIMILARITY.
 CC FT DISULFID 208 221 BY SIMILARITY.
 CC FT CARBOHYD 102 102 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 103 103 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 180 180 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT VARSPLIC 96 113 MISSING (IN ISOFORM NKG2-B).
 CC SO SEQUENCE 233 AA; 26287 MW; 1654BD7958C81A84 CRC64;
 CC
 CC Query Match 18.6%; Score 190; DB 1; Length 233;
 CC Best Local Similarity 27.8%; Pred. No. 5.4e-11;
 CC Matches 55; Conservative 35; Mismatches 86; Indels 22; Gaps 8;
 CC
 CC QY 5 VIYSMLPLPATOANDYGPQKSSSK--PSC-SCLVAITGLTAVL-----SVLLYQ 57
 CC DB 38 IYIAELNLQKASQ---DFQGNDRKTYHCKDLPSEKELVIGLIGLILMASVYTIYVIP 94

```

QY 58 WILCOGNSYST-----CASCPCSPDRMKYGNHCYFVSVEKDNWNSLLEFCLARDSHL 110
DB 95 STLIOHNNSSLNTRRQKARHCHGCHPEWITYSSCYTIGKERETWESLACTSKNSL 154
QY 111 LVITDNOEMSLQVLEAFWICGL-RNNSGWRWEDGSPLEFSR--ISSNFVOTCGAIN 167
DB 155 LSLIDNEEMFLSISPPS--WIGVFRNSSHHPPVTMNGLAFKHEINDSDNAELNCANVLQ 212
QY 168 KNGLOASSCEVPLHGVCK 185
DB 213 VNRLKSACGSSIIYHCK 230

RESULT 5
NKGC_HUMAN STANDARD; PRT; 231 AA.
ID P26717; O43802;
AC 01-AUG-1992 (Rel. 23, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DE 01-MAR-2002 (Rel. 41, Last annotation update)
DE NKG2-C type II integral membrane protein (NKG2-C activating NK
  receptor).
GN KIR2C OR NKG2C.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91178434; PubMed=2007850;
RA Houchens J.P., Yabe T., McSherry C., Bach F.H.;
RT "DNA sequence analysis of NKG2, a family of related cDNA clones
  encoding type II integral membrane proteins on human natural killer
  cells.";
RL J. Exp. Med. 173:1017-1020(1991).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98350122; PubMed=9683661;
RA Glienke J., Sobanov Y., Brostjan C., Steffens C., Nguyen C.,
  Lehrach H., Hofer E., Francis F.;
RT "The genomic organization of NKG2C, E, F, and D receptor genes in the
  human natural killer gene complex.";
RL Immunogenetics 48:163-173(1998).
[3]
RP SEQUENCE FROM N.A.
RX TISSUE=Lymphoid;
RA Blasson R.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PLAYS A ROLE AS A RECEPTOR FOR THE RECOGNITION OF MHC
  CLASS I HLA-E MOLECULES BY NK CELLS AND SOME CYTOTOXIC T-CELLS.
CC -1- SUBUNIT: CAN FORM DISULFIDE-BONDED HETERODIMER WITH CD94.
CC -1- SUBCELLULAR LOCATION: TYPE II membrane protein.
CC -1- TISSUE SPECIFICITY: NATURAL KILLER CELLS.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC
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  or send an email to license@isb-sib.ch).
CC
CC EMBL: X54869; CAA38651.1; -
CC EMBL: AJ001684; CA004922.1; -
CC EMBL: Y13055; CAA73498.1; -
CC PIR: P10374; P10374.
CC MIM: 602891; -
CC InterPro: IPR001304; lectin.c.
CC Pfam: PF00059; lectin.c; 1.
CC SMART: SM00034; CRECT.1.
CC PROSITE: PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
CC PROSITE: PS50041; C_TYPE_LECTIN_2; 1.

```

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KW Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin;
KM Glycoprotein.
FT DOMAIN 1 70 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 71 93 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
  (POTENTIAL).
FT DOMAIN 94 231 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 116 229 C-TYPE LECTIN (LONG FORM).
FT DISULFID 117 128 BY SIMILARITY.
FT DISULFID 145 227 BY SIMILARITY.
FT DISULFID 206 219 BY SIMILARITY.
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 161 161 M->I (IN REF. 1).
SQ SEQUENCE 231 AA; 26072 MW; 6B971EED7542930 CRC64;

Query Match 18.2%; Score 186; DB 1; Length 231;
Best Local Similarity 28.4%; Pred. No. 1.3e-10;
Matches 48; Conservative 31; Mismatches 76; Indels 14; Gaps 5;

QY 24 PQQRSSSKPSCSLVAITGLLAVLLSVLYOIILOGNSYST---CASCPCSPDRW 79
DB 67 PPEKTLAEVLGIICIV-----LMAVTKTVILIPLEQNNSSPNRTQKARHCHGCHPEM 121
QY 80 MKYGNHCYFVSVEKDNWNSLLEFCLARDSHLVTDNOEMSLQVLEAFWICGL-RRN 138
DB 122 IYNSNCYIGKERETWESLACTSKNSLSIDNEEMFLSISPPS--WIGVFRNS 179
QY 139 SGWRWEDGSPLEFSR--ISSNFVOTCGAINKNGLOASSCEVPLHGVCK 185
DB 180 SHHPVVTINGLAFKHKIKDSDNAELNCANVLOVNRKLSACGSSMIYHCK 228

RESULT 6
NKGD_HUMAN STANDARD; PRT; 216 AA.
ID P26718;
AC 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE NKG2-D type II integral membrane protein (NKG2-D activating NK
  receptor).
GN KIR2D OR NKG2D.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91178434; PubMed=2007850;
RA Houchens J.P., Yabe T., McSherry C., Bach F.H.;
RT "DNA sequence analysis of NKG2, a family of related cDNA clones
  encoding type II integral membrane proteins on human natural killer
  cells.";
RL J. Exp. Med. 173:1017-1020(1991).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98350122; PubMed=9683661;
RA Glienke J., Sobanov Y., Brostjan C., Steffens C., Nguyen C.,
  Lehnach H., Hofer E., Francis F.;
RT "The genomic organization of NKG2C, E, F, and D receptor genes in the
  human natural killer gene complex.";
RL Immunogenetics 48:163-173(1998).
CC -1- FUNCTION: PLAYS A ROLE AS A RECEPTOR FOR THE RECOGNITION OF MHC
  CLASS I HLA-E MOLECULES BY NK CELLS AND SOME CYTOTOXIC T-CELLS.
CC -1- SUBUNIT: CAN FORM DISULFIDE-BONDED HETERODIMER WITH CD94.
CC -1- SUBCELLULAR LOCATION: TYPE II membrane protein.
CC -1- TISSUE SPECIFICITY: NATURAL KILLER CELLS.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC
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CC or send an email to license@isb-sib.ch).

DR EMBL: X54870; CAA38652.1; -
DR EMBL: AJ001687; CAA04925.1; -
DR EMBL: AJ001688; CAA04925.1; JOINED.
DR EMBL: AJ001689; CAA04925.1; JOINED.
DR PIR: P03735; P03735.
DR PIR: S19110; S19110.
DR MIM: 602893; -
DR InterPro: IPR001304; lectin_c.
DR Pfam: PF00059; lectin_c.1.
DR SMART: SM00034; CLECT.1.
DR PROSITE: PS00615; C-TYPE_LLECTIN_1; FALSE_NEG.
DR PROSITE: PS50041; C-TYPE_LLECTIN_2; 1.
KW Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin;
KW Glycoprotein.
FT DOMAIN 1 51
FT TRANSMEM 52 72
FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 73 216
FT DOMAIN 98 213
FT DISULFID 99 110
FT DISULFID 127 211
FT DISULFID 189 203
FT CARBOHYD 131 131
FT CARBOHYD 163 163
FT CARBOHYD 202 202
SQ SEQUENCE 216 AA; 25274 MW; C22F6BD53D7800E CRC64;

Query Match 17.6%; Score 180; DB 1; Length 216;
Best Local Similarity 26.8%; Pred. No. 4.4e-10;
Matches 42; Conservative 31; Mismatches 52; Indels 32; Gaps 5;

QY 37 CLVAITLG-----LTFVLLSVLLYQWILCOGNSYSCASCPSPDDRMKGNHCY 88
DB 57 CFLAVAGMIRFTIMVAIWSVFLNSLQEVQIP---LLESTYCGPPKMKWICKKNCYQ 112
QY 89 FSVEEKDNMSLEFCAARDSHLVITDNGMSLQVFLSEAFWIGL---RNNSGRMED 145
DB 113 FPEESKNWYESQSCMSQNSLAKYISKEDDLK--LVSYHMGVLVHPITNSQWMD 170
QY 146 GSPPLNFSRI-----SSNSFVOTGCAIN 167
DB 171 GSILSPNLLTIEMOKDCALVASSFGYIENGSTPN 207

RESULT 7
NKGE_HUMAN STANDARD; PRT; 240 AA.
AC 007444;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE NKGE-E type II integral membrane protein (NKGE-D activating NK
DE receptor).
GN KLRG3 OR NKGE2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-94102823; PubMed-8276468;
RA Adamkiewicz T.V., McSherry C., Bach F.H., Houchins J.P.;
RT "Natural killer lectin-like receptors have divergent carboxy-terminal,
RL distinct from C-type lectins";
RN Immunogenetics 39:218-218(1994).
RN [2]

RP SEQUENCE FROM N.A.
RX MEDLINE-98350122; PubMed-9683661;
RA Glienke J., Sobanov Y., Brostjan C., Steffens C., Nguyen C.,
RA Lennach H., Hofer E., Francis F.;
RT "The genetic organization of NKGC, E, F, and D receptor genes in the
RT human natural killer gene complex";
RL Immunogenetics 48:163-173(1998).
CC -1- FUNCTION: PLAYS A ROLE AS A RECEPTOR FOR THE RECOGNITION OF MHC
CC CLASS I HLA-E MOLECULES BY NK CELLS AND SOME CYTOTOXIC T-CELLS.
CC -1- SUBUNIT: CAN FORM DISULFIDE-BONDED HETERODIMER WITH CD94.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
CC -1- TISSUE SPECIFICITY: NATURAL KILLER CELLS.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.

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CC or send an email to license@isb-sib.ch).

DR EMBL: L14542; AAA1683.1; -
DR EMBL: AJ001685; CAA04923.1; -
DR MIM: 602892; -
DR InterPro: IPR001304; lectin_c.
DR Pfam: PF00059; lectin_c.1.
DR SMART: SM00034; CLECT.1.
DR PROSITE: PS00615; C-TYPE_LLECTIN_1; FALSE_NEG.
DR PROSITE: PS50041; C-TYPE_LLECTIN_2; 1.
KW Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin;
KW Glycoprotein.
FT DOMAIN 1 70
FT TRANSMEM 71 93
FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 94 240
FT DOMAIN 116 230
FT DISULFID 117 128
FT DISULFID 207 220
FT CARBOHYD 100 100
FT CARBOHYD 149 149
FT CARBOHYD 179 179
SQ SEQUENCE 240 AA; 27012 MW; 20691FB21274D8A6 CRC64;

Query Match 17.4%; Score 178.5; DB 1; Length 240;
Best Local Similarity 28.6%; Pred. No. 6.9e-10;
Matches 46; Conservative 30; Mismatches 70; Indels 15; Gaps 6;

QY 24 PQKSSSKPSCCLVATLGLLAVLSVLLYQWILCOGNSYSCASCPSPDDRM 79
DB 67 PPKRLTAEVLGIIIV-----LMAIVLTKTIVLIPLEQNNSSPNRTQKARPCGCPPEW 121
QY 80 MKYGNHCYFVEEKNMSLEFCAARDSHLVITDN--QEMSLQVFLSEAFWIGL--RN 137
DB 122 ITYSNCTYIKERKRYWESLQACASKNSSSLSDNEEKFKLASILPSS--WIGVERN 179
QY 138 NSGWRMGSPPLNFSR--ISSNSFVOTGCAINKGLQASSC 176
DB 180 SSMHPWTINLAKRHEIKSDHAEKNCMLHVGSLISDQC 220

RESULT 8
NK13_RAT STANDARD; PRT; 223 AA.
AC P27471;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Natural killer cell surface protein P1-3.2.3 (NKR-P1 3.2.3) (Antigen
DE 3.2.3).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90378305; PubMed=2399464;
 RA Georgia R., Rudert M.A., Vavassori C., Chambers W.H.,
 RT Hiseirodt J.C., Trucco M.,
 RL "NKR-PI, a signal transduction molecule on natural killer cells."
 CC Science 249:1298-1300(1990).
 CC -1- FUNCTION: MEDIATES TRANSMEMBRANE SIGNALING IN NATURAL KILLER
 CC (NK) CELLS. AND SO MAY ACT AS A RECEPTOR ABLE TO SELECTIVELY
 CC TRIGGER NK CELL ACTIVITY.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
 CC -1- TISSUE SPECIFICITY: NATURAL KILLER CELLS.
 CC -1- MISCELLANEOUS: LIGAND BINDING MAY BE CALCIUM DEPENDENT.
 CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL, M62891; AAA41710.1; -.
 DR PIR, A35917; A35917.
 DR InterPro: IPR001304; lectin_c.
 DR Pfam: PF00059; lectin_c; 1.
 DR SMART: SM00034; CLECT; 1.
 DR PROSITE: PS00615; C-TYPE_LECTIN_1; FALSE_NEG.
 DR PROSITE: PS50041; C-TYPE_LECTIN_2; 1.
 DR GlycoProtein: Antigen; Transmembrane; Signal-anchor; Lectin.
 KW DOMAIN 1 43 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 44 63 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT DOMAIN 64 223 EXTRACELLULAR (POTENTIAL).
 FT DISULFID 93 212 C-TYPE LECTIN (LONG FORM).
 FT DISULFID 94 105 BY SIMILARITY.
 FT DISULFID 122 210 BY SIMILARITY.
 FT CARBOHYD 189 202 BY SIMILARITY.
 FT CARBOHYD 82 82 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 169 169 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 223 AA; 24551 MW; FCD12B212DDF4330 CRC64;

Query Match 17.2%; Score 175.5; DB 1; Length 223;
 Best Local Similarity 27.1%; Pred. No. 1.2e-09;
 Matches 49; Conservative 44; Mismatches 67; Indels 21; Gaps 9;

QY 24 PQQSSSSKSSCSGLVAITGLL-TAVLLSVLYRQ-----WILCOGSNSTCASCPS-- 74
 DB 35 PRSHRLALTKSCAGLILLYLALVAGMSILVYVQKPSVPERVLQ-ENLSKTGS-PKLL 92
 QY 75 -CPDRMKYGNHCYFVSVEEKDMSLFECLARDSHLLVITDQEMSLLOYF--LISAF 130
 DB 93 KCPEDMISHRDCKPHVQSTSTWKESLADCGKGATILLVQDELETRLRMLTKRISSSF 152
 QY 131 CWIGLR--NNSGRWMDGSLFNS--RISNSVFOVCGAIKNGKGLAASCEVPLHGCK 185
 DB 153 -WIGLSTYLSDENMKWINGSTLNSDVLSTGDTEDKSCASVSODKVLSECDSDNIWCO 211
 QY 186 K 186
 DB 212 K 212

RESULT 9
 MMGL MOUSE STANDARD; PRT; 304 AA.
 AC P49300; .

DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Macrophage asialoglycoprotein-binding protein (M-ASGP-BP) (Macrophage
 DE galactose/N-acetylgalactosamine-specific lectin) (MMGL).
 GN MGL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C3H/HEN;
 RX MEDLINE=92268032; PubMed=1587794;
 RA Sato M., Kawakami K., Osawa T., Toyoshima S.,
 RT "Molecular cloning and expression of cDNA encoding a galactose/N-
 RT acetylgalactosamine-specific lectin on mouse tumoricidal
 RT macrophages."
 RL J. Biochem. 111:331-336(1992).
 RN [2]
 RP SEQUENCE OF 102-120 AND 137-151.
 RC STRAIN=C3H/HEN;
 RX MEDLINE=89197865; PubMed=3241002;
 RA Oda S., Sato M., Toyoshima S., Osawa T.;
 RT "Purification and characterization of a lectin-like molecule specific
 RT for galactose/N-acetyl-galactosamine from tumoricidal macrophages."
 RL J. Biochem. 104:600-605(1988).
 CC -1- FUNCTION: RECOGNIZES TERMINAL GALACTOSE AND N-ACETYL GALACTOSAMINE
 CC UNITS. MAY PARTICIPATE IN THE INTERACTION BETWEEN TUMORICIDAL
 CC MACROPHAGES AND TUMOR CELLS.
 CC -1- SUBUNIT: HOMO-OLIGOMER.
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
 CC -1- TISSUE SPECIFICITY: IS EXPRESSED ON THE SURFACE OF ACTIVATED
 CC MACROPHAGES.
 CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
 CC -----
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 CC -----
 DR EMBL, S36676; AAB22171.1; -.
 DR HSSP: P06734; IKJE.
 DR MGD: MGI:96975; MGI.
 DR InterPro: IPR001304; lectin_c.
 DR Pfam: PF00059; lectin_c; 1.
 DR SMART: SM00034; CLECT; 1.
 DR PROSITE: PS00615; C-TYPE_LECTIN_1; 1.
 DR PROSITE: PS50041; C-TYPE_LECTIN_2; 1.
 KW Lectin; Glycoprotein; Transmembrane; Calcium; Signal-anchor.
 FT TRANSMEM 1 35 CYTOPLASMIC (POTENTIAL).
 FT (POTENTIAL).
 FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT DOMAIN 36 56 EXTRACELLULAR (POTENTIAL).
 FT DISULFID 57 304 C-TYPE LECTIN (LONG FORM).
 FT DISULFID 172 298 BY SIMILARITY.
 FT DISULFID 173 184 BY SIMILARITY.
 FT DISULFID 201 296 BY SIMILARITY.
 FT DISULFID 274 288 BY SIMILARITY.
 FT CARBOHYD 74 74 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 74 74 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 304 AA; 34596 MW; 3F79CD12C34F5BCC CRC64;

Query Match 17.1%; Score 174.5; DB 1; Length 304;
 Best Local Similarity 27.5%; Pred. No. 2.1e-09;
 Matches 39; Conservative 27; Mismatches 61; Indels 15; Gaps 5;

QY 59 ILCOGSNSTCASC-CPSPDRMKYGNHCYFVSVEEKDMSLFECLARDSHLLVITDQ 117
 DB 156 LTCOLANLKNNGSEVACCPPLHWTREHSGCYWFSEKSPFADKTCRLNLSLVVNSLE 215

OC Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxId=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=90378305; Pubmed=2399464;
 RA Giorda R., Rudert W.A., Vavasori C., Chambers W.H.,
 RA Hiserodt J.C., Trucco M.:
 RT "NKR-PL, a signal transduction molecule on natural killer cells.",
 RT Science 249:1298-1300(1990).
 CC -1- FUNCTION: MEDIATES TRANSMEMBRANE SIGNALING IN NATURAL KILLER
 CC (NK) CELLS. AND SO MAY ACT AS A RECEPTOR ABLE TO SELECTIVELY
 CC TRIGGER NK CELL ACTIVITY.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
 CC -1- TISSUE SPECIFICITY: NATURAL KILLER CELLS.
 CC -1- MISCELLANEOUS: LIGAND BINDING MAY BE CALCIUM DEPENDENT.
 CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
 CC -----
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 CC -----
 CC EMBL; M62891; AAA1710.1; -.
 DR PIR; A35917; A35917.
 DR InterPro; IPR001304; lectin_c.
 DR Pfam; PF00059; lectin_c; 1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C-TYPE_LECTIN_1; FALSE_NEG.
 DR PROSITE; PS50041; C-TYPE_LECTIN_2; 1.
 DR GlycoProtein; Antigen; Transmembrane; Signal-anchor; Lectin.
 KW DOMAIN 1 43 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 44 63 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT 43 (POTENTIAL).
 FT 63 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 64 223 C-TYPE LECTIN (LONG FORM).
 FT DISULFID 93 212 BY SIMILARITY.
 FT DISULFID 94 105 BY SIMILARITY.
 FT DISULFID 122 210 BY SIMILARITY.
 FT DISULFID 189 202 BY SIMILARITY.
 FT CARBOHYD 82 82 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 169 169 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 169 169 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 223 AA; 24551 MW; FCD12B212DDF4330 CRC64;

 Query Match 17.2%; Score 175.5; DB 1; Length 223;
 Best Local Similarity 27.1%; Pred. No. 1.2e-09;
 Matches 49; Conservative 44; Mismatches 67; Indels 21; Gaps 9;
 OY 24 PQQSSSSRPSQCLVAITGLL-TAVLLSVLYQ-----WILGGSNYSTCASCPS-- 74
 DB 35 PRSHRLATKSCAGLILVLAVALGMSILVAVLQKPSVECRVLIQ-ENLSKTS-PAKL 92
 OY 75 -CPDRMKYGNHCYFSVEEKDNSSLEFLARDSHLLVTTDQMSILOV---LESAF 130
 DB 93 KCPKDWLSHRDKCFHVSQTSITWKESLADCGKGATLLVODDELRFLRLTRKRISSE 152
 OY 131 CWGLR---NSGWRWEDGSPLPFS--RISNSFVOTCGAIKNGLOASSEVPLHGVCK 185
 DB 153 -WIGSLYTLSDENMKWINGSTLNSDVLSTIGDPEKDCASVSODKVLSESCDSNIMVQ 211
 OY 186 K 186
 DB 212 K 212
 RESULT 9
 MAGL_MOUSE STANDARD; PRT; 304 AA.
 AC P49300;

DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Macrophage asialoglycoprotein-binding protein (M-ASGP-BP) (Macrophage
 DE galactose/N-acetylgalactosamine-specific lectin) (MGL).
 GN MGL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C3H/HEN;
 RX MEDLINE=92268032; Pubmed=1587794;
 RA Sato M., Kawakami K., Osawa T., Toyoshima S.;
 RT "Molecular cloning and expression of cDNA encoding a galactose/N-
 RT acetylgalactosamine-specific lectin on mouse tumoricidal
 RT macrophages.";
 RL J. Biochem. 111:331-336(1992).
 RN [2]
 RP SEQUENCE OF 102-120 AND 137-151.
 RC STRAIN=C3H/HEN;
 RX MEDLINE=89197865; Pubmed=3241002;
 RA Oda S., Sato M., Toyoshima S., Osawa T.;
 RT "Purification and characterization of a lectin-like molecule specific
 RT for galactose/N-acetyl-galactosamine from tumoricidal macrophages.";
 RL J. Biochem. 104:600-605(1988).
 CC -1- FUNCTION: RECOGNIZES TERMINAL GALACTOSE AND N-ACETYLGALACTOSAMINE
 CC UNITS. MAY PARTICIPATE IN THE INTERACTION BETWEEN TUMORICIDAL
 CC MACROPHAGES AND TUMOR CELLS.
 CC -1- SUBUNIT: HOMO-OLIGOMER.
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
 CC -1- TISSUE SPECIFICITY: IS EXPRESSED ON THE SURFACE OF ACTIVATED
 CC MACROPHAGES.
 CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; S36676; AAB22171.1; -.
 DR HSSP; P06734; IKCE.
 DR MGI; MGI:96975; Mgl.
 DR InterPro; IPR001304; lectin_c.
 DR Pfam; PF00059; lectin_c; 1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C-TYPE_LECTIN_1; 1.
 DR PROSITE; PS50041; C-TYPE_LECTIN_2; 1.
 KW Lectin; Glycoprotein; Transmembrane; Calcium; Signal-anchor.
 FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT 56 (POTENTIAL).
 FT DOMAIN 57 304 EXTRACELLULAR (POTENTIAL).
 FT DISULFID 172 298 C-TYPE LECTIN (LONG FORM).
 FT DISULFID 173 184 BY SIMILARITY.
 FT DISULFID 201 296 BY SIMILARITY.
 FT DISULFID 274 288 BY SIMILARITY.
 FT CARBOHYD 74 74 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 304 AA; 34596 MW; 3F79CD12C34F5BC CRC64;

 Query Match 17.1%; Score 174.5; DB 1; Length 304;
 Best Local Similarity 27.5%; Pred. No. 2.1e-09;
 Matches 39; Conservative 27; Mismatches 61; Indels 15; Gaps 5;
 OY 59 ILGGSNYSSTCAS-CPSPDRMKYGNHCYFSVEEKDNSSLEFLARDSHLLVTTDQ 117
 DB 156 LTCQLANLKNNGSEVACPLHMTHEGSCYIFSESEKSPENDKCYRLNLSLVVNSLE 215

QY 118 EMLLOYFLSEAFWIGLRRNSG--WRMEDGSP...-NFSRISNSPV-----QNGC 164
 DB 216 EONLORLRLANVWVIGLITDNGPWRWDGTFDEKFKRMALPDNNFGLGSGEDCA 275
 QY 165 AINKNG-LQASCEVPLHGVCK 185
 DB 276 HITGGPMNDVCCQRTFRWICE 297

RESULT 10
 ID CD69_HUMAN STANDARD; PRT; 199 AA.
 AC 007108:
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-OCT-1994 (Rel. 40, Last annotation update)
 DE Early activation antigen CD69 (Early T-cell activation antigen p60)
 DE (GP32/28) (Leu-23) (MLR-3) (EAL) (BL-AC/P26) (Activation inducer
 DE molecule) (A1M).
 GN CD69.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=93340630; PubMed=8496594;
 RA Hamann J., Fiebig H., Strauss M.,
 RT Expression cloning of the early activation antigen CD69, a type II
 RT integral membrane protein with a C-type lectin domain.";
 RL J. Immunol. 150:4920-4927(1993).
 RN [2]
 RP SEQUENCE FROM N.A. AND SEQUENCE OF 96-103; 128-146 AND 189-199.
 RC TISSUE=Blood;
 RX MEDLINE=93340630; PubMed=8340758;
 RA Lopez-Cabrera M., Santis A.G., Fernandez-Ruiz E., Blacher R.,
 RA Esch F., Sanchez-Mateos P., Sanchez-Madrid F.,
 RT "Molecular cloning, expression, and chromosomal localization of the
 RT human earliest lymphocyte activation antigen A1M/CD69, a new member
 RT of the C-type animal lectin superfamily of signal-transmitting
 RT receptors.";
 RL J. Exp. Med. 178:537-547(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93314711; PubMed=8100776;
 RA Ziegler S.F., Ramsdell F., Hjertild K.A., Armitage R.J.,
 RA Grabstein K.H., Hennen K.B., Farrar T., Fanslow W.C., Shevach E.M.,
 RA Alderson M.R.,
 RT "Molecular characterization of the early activation antigen CD69: a
 RT type II membrane glycoprotein related to a family of natural killer
 RT cell activation antigens.";
 RL Eur. J. Immunol. 23:1643-1648(1993).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=94298875; PubMed=8026529;
 RA Santis A., Lopez-Cabrera M., Hamann J., Strauss M., Sanchez-Madrid F.,
 RT "Structure of the gene coding for the human early lymphocyte
 RT activation antigen CD69: a C-type lectin receptor evolutionarily
 RT related with the gene families of natural killer cell-specific
 RT receptors.";
 RL Eur. J. Immunol. 24:1692-1697(1994).
 CC -1- FUNCTION: INVOLVED IN LYMPHOCYTE PROLIFERATION AND FUNCTIONS AS A
 CC SIGNAL TRANSMITTING RECEPTOR IN LYMPHOCYTES, NATURAL KILLER (NK)
 CC CELLS, AND PLATELETS.
 CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
 CC -1- TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T CELLS,
 CC B-CELLS, NATURAL KILLER CELLS, NEUTROPHILS, EOSINOPHILS, EPIDERMAL
 CC LANGERHANS CELLS AND PLATELETS.
 CC -1- DEVELOPMENTAL STAGE: EARLIEST INDUCIBLE CELL SURFACE GLYCOPROTEIN

CC ACQUIRED DURING LYMPHOID ACTIVATION.
 CC -1- INDUCTION: BY ANTIGENS, MITOGENS OR ACTIVATORS OF PKC ON THE
 CC SURFACE OF T AND B LYMPHOCYTES. BY INTERACTION OF IL-2 WITH THE
 CC P/75 IL-2R ON THE SURFACE OF NK CELLS.
 CC -1- PTM: CONSTITUTIVE SER/THR PHOSPHORYLATION IN BOTH MATURE
 CC THYMOCYTES AND ACTIVATED T LYMPHOCYTES.
 CC -1- DATABASE: NAME=PROV; NOTE=CD guide CD69 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd69.htm".
 CC -----
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 CC -----
 CC DR EMBL; L07555; AAB46359.1; -;
 CC DR EMBL; Z22576; CAA80298.1; -;
 CC DR EMBL; Z30426; CAA83017.1; -;
 CC DR EMBL; Z30430; CAA83017.1; JOINED.
 CC DR EMBL; Z30427; CAA83017.1; JOINED.
 CC DR EMBL; Z30429; CAA83017.1; JOINED.
 CC DR EMBL; Z30428; CAA83017.1; JOINED.
 CC DR PIR; JH0822; JH0822.
 CC DR MIM; 107273; -;
 CC DR InterPro; IPR001304; lectin_c.
 CC DR Pfam; PF00059; lectin_c; 1.
 CC DR SMART; SM00034; CLECT; 1.
 CC DR PROSITE; PS00615; C-TYPE LECTIN_1; FALSE_NEG.
 CC DR PROSITE; PS50041; C-TYPE LECTIN_2; 1.
 CC KW Antigen; B-cell; Glycoprotein; Transmembrane; Lectin; Signal-anchor;
 CC Phosphorylation.
 CC FT DOMAIN 1 40 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 1 61 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 CC FT DOMAIN 62 199 (POTENTIAL).
 CC FT DOMAIN 67 199 EXTRACELLULAR (POTENTIAL).
 CC FT DISULFID 68 85 C-TYPE LECTIN (LONG FORM).
 CC FT DISULFID 96 194 BY SIMILARITY.
 CC FT DISULFID 173 186 BY SIMILARITY.
 CC FT CARBOHYD 166 166 N-LINKED (GLCNAC...) (POTENTIAL).
 CC SQ SEQUENCE 199 AA; 22559 MW; 172E269D2F8BDFB CRC64;

Query Match 17.0%; Score 174; DB 1; Length 199;
 Best Local Similarity 22.9%; Pred. No. 1.5e-09;
 Matches 40; Conservative 33; Mismatches 76; Indels 26; Gaps 5;

QY 30 SSKPSCGLVATITGLALVAVLSVLLYOMILCOGSNYSCASC-----SC 75
 DB 30 STRHEGSRQVPLCAVMWVFTITLIALLSVGQY-----NCPQGYFSPMSDSHVSSC 85
 QY 76 PDRMKYGNHCYFSEVERKDNNSLEPCLRDASHLVITDNGEMSLLOYFLSEAFWIGL 135
 DB 86 SEDWVGYQRCYFTISTYKRSMTSAQNACSEHGATLAVIDSEKDNMFLKYAREEHVGL 145
 QY 136 RNNSG--WRMEDGSP...-NFSRISNSPVOTCGAINKNGLAQASCEVPLHGVCK 186
 DB 146 KKEPGHPKMSNGKRFNNMFWNTGSDK---CVFLKNTEVSSMECEKNLWICNK 196

RESULT 11
 ID CLF2_HUMAN STANDARD; PRT; 149 AA.
 AC 092478:
 DT 01-MAR-2002 (Rel. 41, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE C-type lectin superfamily member 2 (Activation-induced C-type lectin).
 GN CLEC2 OR ATCL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;


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OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97190245; PubMed=9038101;
RA Hamann J., Montomery K.T., Lau S., Kucheraipati R., van Lier R.A.W.;
RT "NICL, a new activation induced antigen encoded by the human NK gene
  complex.",
  Immunogenetics 45:295-300(1997).
RL Immunogenetics 45:295-300(1997).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Probable).
CC -1- TISSUE SPECIFICITY: Expressed preferentially in lymphoid tissues,
  and in most hematopoietic cell types.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -----
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CC -----
DR EMBL: X96719; CAA65480.1; .
DR MIM: 603242; .
DR InterPro: IPR001304; lectin_c.
DR Pfam: PF00059; lectin_c; 1.
DR SMART: SM00034; CLECT; 1.
DR PROSITE: PS00615; C-TYPE_LECTIN_1; FALSE_NEG.
DR PROSITE: PS50041; C-TYPE_LECTIN_2; 1.
KM Glycoprotein; Transmembrane; Lectin; Signal-anchor.
FT DOMAIN 1 7
FT TRANSMEM 8 25
FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
  (POTENTIAL).
FT DOMAIN 26 149
FT EXTRACELLULAR (POTENTIAL).
FT DOMAIN 42 145
FT C-TYPE LECTIN.
FT DISULFID 46 63
FT BY SIMILARITY.
FT DISULFID 87 144
FT BY SIMILARITY.
FT DISULFID 123 136
FT BY SIMILARITY.
FT CARBOHYD 57 57
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 62 62
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 100 100
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 149 AA; 17329 MW; 0B4FE2EC7EB36C55 CRC64;

Query Match 16.4%; Score 168; DB 1; Length 149;
Best Local Similarity 31.3%; Pred. No. 4e-09;
Matches 36; Conservative 24; Mismatches 49; Indels 6; Gaps 3;

OY 75 CPDMMKYGNCYFSEVKEKDNSSLEFCIARDSHLYITDQMSLLOVFLSEAFQWIG 134
  ||| : : : ||||| ||||| : : : : : : : : : : : : : : : : : :
DB 35 CPYDMIGQNKCYFSEKEDGNSSKYNCSYOHADLTITDNEENPLRRYKCSSDHWIG 94

OY 135 L--RNNSGMWMEDGSPUNFSRISNSFVONCGAINKNGLOASCEVPLHGVCCK 186
  | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
DB 95 LKMAKNRIG-QWVHGA--TFTRKSPGMRSGECAYLSDGGAARARCYTERKWKCRK 146

RESULT 12
LECT MOUSE STANDARD; PRT; 301 AA.
AC P24721;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Asialoglycoprotein receptor 2 (Hepatic lectin 2) (MHL-2) (ASGP-R)
  (ASGP-R).
GN ASGR2 OR ASGR-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=C57BL/6; TISSUE=Liver;
RX MEDLINE=91027942; PubMed=2223888;
RA Sanford J.P., Doyle D.;
RT "Mouse asialoglycoprotein receptor cDNA sequence: conservation of
  receptor genes during mammalian evolution.",
  Biochim. Biophys. Acta 1087:259-261(1990).
RL Biochim. Biophys. Acta 1087:259-261(1990).
CC -1- FUNCTION: MEDIATES THE ENDOCYTOSIS OF PLASMA GLYCOPROTEINS TO
  WHICH THE TERMINAL SIALIC ACID RESIDUE ON THEIR COMPLEX
  CARBOHYDRATE MOIETIES HAS BEEN REMOVED. THE RECEPTOR RECOGNIZES
  TERMINAL GALACTOSE AND N-ACETYLGALACTOSAMINE UNITS. AFTER LIGAND
  BINDING TO THE RECEPTOR, THE RESULTING COMPLEX IS INTERNALIZED AND
  TRANSPORTED TO A SORTING ORGANELLE, WHERE RECEPTOR AND LIGAND ARE
  DISASSOCIATED. THE RECEPTOR THEN RETURNS TO THE CELL MEMBRANE
  SURFACE.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
CC -1- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN HEPATIC PARENCHYMAL
  CELLS.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -----
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CC -----
DR EMBL: X53042; CAA37211.1; .
DR PIR: S13165; S13165.
DR HSSP: P06734; 1KJE.
DR MGD: MGI:88082; Asgr2.
DR InterPro: IPR001304; lectin_c.
DR Pfam: PF00059; lectin_c; 1.
DR SMART: SM00034; CLECT; 1.
DR PROSITE: PS00615; C-TYPE_LECTIN_1; .
DR PROSITE: PS50041; C-TYPE_LECTIN_2; 1.
KM Lectin; Glycoprotein; Receptor; Endocytosis; Transmembrane;
  Calcium; Signal-anchor; Phosphorylation.
FT DOMAIN 1 58
FT TRANSMEM 59 79
FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
  (POTENTIAL).
FT DOMAIN 80 301
FT EXTRACELLULAR (POTENTIAL).
FT DOMAIN 169 295
FT C-TYPE LECTIN (LONG FORM).
FT DISULFID 170 181
FT BY SIMILARITY.
FT DISULFID 198 293
FT BY SIMILARITY.
FT DISULFID 271 285
FT BY SIMILARITY.
FT CARBOHYD 97 97
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 165 165
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 298 298
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 301 AA; 34907 MW; 3A29F1AFBA68F298 CRC64;

Query Match 16.3%; Score 167; DB 1; Length 301;
Best Local Similarity 25.9%; Pred. No. 1.1e-08;
Matches 55; Conservative 29; Mismatches 72; Indels 56; Gaps 9;

OY 27 KSSSKRSPSCSLVAI---TIGLITAVLL-----SVLLT----- 56
  | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
DB 92 KETFSNFSSSTLMFEGALDTLGSTNAIITSWLAQLEEKQOOLKADHSTLFLFKHPMD 151

OY 57 -QWILCO-----GSNYSTGASCSPSPDRMMKYGNHCYFSEVKEKDNSSLEFCIARDSHLL 111
  ||| : : : ||||| ||||| : : : : : : : : : : : : : : : : : :
DB 152 LFTLTCQALVFOFSGNGEC-----CPVNWFEFGSCWFSRBDGLTWAEADQYCOLFNHLL 206

OY 112 VITDQMSILQVFLSEAFQWIGLGRNNSG-WRMEDGSPUNFSRISNSFVQ----- 161
  ||| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
DB 207 VINSREDDFVYKHSQFIMWIGLIDRDGSKWKVQSDYDR-SYRWKATFQPDNMGGHQ 265

OY 162 ---TCGALINKG-LQASCEVPLHGVCCKVR 188
  | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
DB 266 GGGEPCAEITLSDGHMNDNFCQOVNRMVCEKRR 297

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DR   MGD: MG1:101907; Klr1a1.
DR   InterPro: IPR001304; Lectin_C.
DR   Pfam: PF00059; Lectin_c; 1.
DR   SMART: SM00034; CLECT; 1.
DR   PROSITE: PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
DR   PROSITE: PS50041; C_TYPE_LECTIN_2; 1.
KM   T-cell; Glycoprotein; Antigen; Transmembrane; Cell adhesion;
KW   Signal-anchor; Lectin; Receptor; Multiene family.
FT   DOMAIN 1 44
FT   TRANSMEM 45 66
FT   DOMAIN 67 262
FT   DOMAIN 138 257
FT   DISULFID 167 253
FT   DISULFID 232 245
FT   SITE 137 139
FT   CARBOHYD 86 86
FT   CARBOHYD 103 103
FT   CARBOHYD 123 123
FT   CONFLICT 76 78
FT   CONFLICT 106 106
FT   CONFLICT 166 166
FT   CONFLICT 223 223
SQ   SEQUENCE 262 AA; 30498 MW; 3C3328D265F71B5E CRC64;
      IREAVLLS 52
      5 VYEMLEPRTATQANDYGPQOKSSSKSPS---CSC--LVAILTG-----LTVAVLLS 52
      6 VTYSMVRFHKSAGLQKQVRETPGPRPAGYRRCSPFHWKFTVIALGIFCFLLLVAVSVA 65
      79 -----ILCOGSNYSTCASCPSCPPDR-----
      53 VLTQW-----
      66 IKIQYDQOKNCEFLNHNHNCSSMOSDINLKDMLNKSIECDLLESLNBDQNRLYNKT 125
      79 -----WMKYGNHCYFYSVEKEDMNSLFECLARDSHLAVITDQNSL 121
      126 KTVLDSLOHTGRGDQKYVWFECYGMKCYFYFMDRKRTWSGCKACQSSSLTKIDDEDELKF 185
      122 LQVFLSAFCWIGL---RNSGMRWEGSPINFRISNSFVOT-----CGAINKNGLOA 173
      186 LQLVVPSDSCWVGSLSYDNKKKKDMAMIDNRP---SKLALNTGKYNIRDGGCMILSKTRLDN 242
      174 SSCEVPLHGVCCK 186
      243 GNCDOVFICIGCK 255

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OM protein - protein search, using sw model

Run on: September 9, 2002, 14:41:21 ; Search time 13.1 Seconds

(without alignments)
352,400 Million cell updates/sec

Title: US-09-811-367b-1

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued_Patents_AA.*

1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PCrus.COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/Backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	525.5	51.4	188	3	US-08-722-126A-5
2	525.5	51.4	188	3	PCT-US95-04258-5
3	370.5	36.2	114	3	US-08-722-126A-6
4	370.5	36.2	114	5	PCT-US95-04258-6
5	201	19.6	225	2	US-08-738-462-2
6	201	19.6	225	5	PCT-US94-07587-2
7	196.5	19.2	179	1	US-08-690-095-9
8	196.5	19.2	179	2	US-08-650-578-2
9	196.5	19.2	179	2	US-08-688-342-3
10	196.5	19.2	179	2	US-09-113-789-3
11	196.5	19.2	179	3	US-09-113-789-9
12	196.5	19.2	199	5	PCT-US93-10418-4
13	193	18.9	270	2	US-09-055-095-4
14	193	18.9	270	2	US-08-809-494A-2
15	193	18.9	270	4	US-09-352-302-2
16	193	18.9	273	4	US-08-809-494A-4
17	193	18.9	273	4	US-09-352-302-4
18	190	18.6	233	1	US-08-690-095-8
19	190	18.6	233	4	US-09-113-789-8
20	190	18.6	233	4	US-08-543-246B-2
21	190	18.6	233	4	US-08-543-246B-21
22	185.5	18.1	316	4	US-09-111-470-4
23	184	18.0	215	3	US-08-690-095-7
24	184	18.0	215	3	US-09-113-789-7
25	184	18.0	215	4	US-08-543-246B-16
26	184	18.0	215	4	US-08-543-246B-22
27	182	17.8	231	1	US-08-690-095-6

28	182	17.8	231	3	US-09-113-789-6	Sequence 6, Appl
29	182	17.8	231	4	US-08-543-246B-6	Sequence 6, Appl
30	182	17.8	231	4	US-08-543-246B-23	Sequence 23, Appl
31	181	17.7	273	2	US-09-055-095-3	Sequence 3, Appl
32	181	17.7	273	2	US-08-809-494A-6	Sequence 6, Appl
33	181	17.7	273	4	US-09-352-302-6	Sequence 9, Appl
34	180	17.6	216	4	US-08-543-246B-9	Sequence 9, Appl
35	180	17.6	216	4	US-08-543-246B-24	Sequence 24, Appl
36	179.5	17.5	273	4	US-09-111-470-10	Sequence 10, Appl
37	179.5	17.5	292	2	US-08-688-342-4	Sequence 4, Appl
38	179.5	17.5	292	2	US-09-113-788-4	Sequence 4, Appl
39	175.5	17.2	168	3	US-08-772-440-17	Sequence 17, Appl
40	175.5	17.2	201	2	US-08-688-342-1	Sequence 1, Appl
41	175.5	17.2	201	2	US-09-113-788-1	Sequence 1, Appl
42	174	17.0	199	5	PCT-US93-10418-2	Sequence 2, Appl
43	173	16.9	175	3	US-08-772-440-15	Sequence 15, Appl
44	173	16.9	209	3	US-08-772-440-4	Sequence 4, Appl
45	172	16.8	134	3	US-08-772-440-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-08-722-126A-5
; Sequence 5, Application US/08722126A
; Patent No. 6034227
; GENERAL INFORMATION:
; APPLICANT: PECHT, Israel
; APPLICANT: GUTHMANN, Marcelo D.
; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
; TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA).
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,126A
; FILING DATE: 08-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04258
; FILING DATE: 06-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 109257
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: PECHT-1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-722-126A-5
Query Match 51.4%; Score 525.5; DB 3; Length 188;

RESULT 4
PCT-US95-04258-6
Sequence 6, Application PC/TUS9504258
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419, Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04258
FILING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 109257
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: PECHT-1 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-04258-6

Query Match 36.2%; Score 370.5; DB 5; Length 114;
Best Local Similarity 58.4%; Pred. No. 1.5e-32;
Matches 66; Conservative 18; Mismatches 28; Indels 1; Gaps 1;

QY 75 CPBRMKGHCYFSEYEDKWNLSLEFCLARDSHLLVITPDNOMSLQVFLSEAFWIG 134
DB 1 CPNLMWNSHCHYFSEYEDKWNLSLEFCLARDSHLLVITPDNOMSLQVFLSEAFWIG 60

QY 135 LRNNGGWRMGDSPLNFSRISNSFVOTCGAINKNGLOASSCEVPLHGCVCKV 187
DB 61 LRDDGWRMGDSPLNFSRISNSFVOTCGAINKNGLOASSCEVPLHGCVCKV 112

RESULT 5
US-08-738-462-2
Sequence 2, Application US/08738462
Patent No. 5965401
GENERAL INFORMATION:
APPLICANT: Chang, Chiwen
APPLICANT: Lanier, Lewis L.
APPLICANT: Phillips Jr., Joseph H.
TITLE OF INVENTION: Purified Mammalian NK Antigen and
TITLE OF INVENTION: Related Reagents
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNA Research Institute
STREET: 901 California Avenue
CITY: Palo Alto

STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,462
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/093,435
FILING DATE: 16-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Chang, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0397
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-738-462-2

Query Match 19.6%; Score 201; DB 2; Length 225;
Best Local Similarity 26.0%; Pred. No. 6.2e-14;
Matches 58; Conservative 36; Mismatches 81; Indels 48; Gaps 8;

QY 1 MTDVYSMLPRTAONDYGPQKSSSKP-----SCSCVAITIG 44
DB 1 MDQAIYALMLPT-----DSGPSSPSLPRDVCQSPWHPALKSCAGITLV- 53

QY 45 LTFVILSVLYOWILCOGSNYSFCA-----SCSPCDRMKYGHCYFS 90
DB 54 VVTGLSVST-----SLIKSSIEKCSVDIQSRNKTTERPGLINCFYMOQLREKCLFS 109

QY 91 VEKDNMSLEFCLARDSHLLVITPDNOMSLQVFLSE--AFCWIGLR--NNSGWRMGD 145
DB 110 HTVNMWNSLADCSFKESLLIRKDELHTQNLIRKAILFWIGLNFSLSEKMWKWIN 169

QY 146 GSPLNF--RISNSFVOTCGAINKNGLOASSCEVPLHGCVCK 186
DB 170 GSPLNSNLEIRGDAKENSICISISQTSYSEYCSFEIRWICK 212

RESULT 6
PCT-US94-07587-2
Sequence 2, Application PC/TUS9407587
GENERAL INFORMATION:
APPLICANT: Schering Corp.
TITLE OF INVENTION: PURIFIED MAMMALIAN NK ANTIGENS AND
TITLE OF INVENTION: RELATED REAGENTS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering Corp.
STREET: One Giralda Farms
CITY: Madison
STATE: New Jersey
COUNTRY: USA
ZIP: 07940
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/07587
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Lunn, Paul G.
 REGISTRATION NUMBER: 32,743
 REFERENCE/DOCKET NUMBER: DX0397K
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-822-7255
 TELEFAX: 201-822-7039
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 225 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US94-07587-2

Query Match 19.6%; Score 201; DB 5; Length 225;
 Best Local Similarity 26.0%; Pred. No. 6.2e-14;
 Matches 58; Conservative 36; Mismatches 81; Indels 48; Gaps 8;

QY 1 MTDVITSMELPRTAQNNDYGPQKSSSKP-----SCSCVAITLG 44
 DB 1 MDQAIYAEINLPT-----DSGPSSPSLPDVCQSPWHOFALKSCAGIILVL- 53
 QY 45 LTPAVLSVLLYQWILCOGSMYSCA-----SCSPCDRMKRYGNHCYFS 90
 DB 54 VVTGLSVST-----SLQKSIKCSVDIQSRNKTTPGILNPIYQGLRECLLF 109
 QY 91 VEEDKMSLEFCLARDSHLIVTDNOMSLQVFLSE--APCWIGLR---NNSGWRMD 145
 DB 110 HTVPMNNNSLDSCSTKESLLIRDKDELHTQNLIRKALLFWIGLNFSLSEKMKWIN 169
 QY 146 GSPNFS--RISSNSFVOTGAIKNGKQASSCEVPLHGCK 186
 DB 170 GSPNFSNDELTRGDKNKSCISOTSVSEYCTEIRWICK 212

RESULT 7

US-08-690-095-9

Sequence 9, Application US/08660095
 Patent No. 5792648
 GENERAL INFORMATION:
 APPLICANT: Hillman, Jennifer L.
 APPLICANT: Au-Young, Janice
 APPLICANT: Goli, Surya K.
 TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: U.S.
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/690,095
 FILING DATE: Filed Herewith
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0110 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166
 INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:
 LENGTH: 179 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 IMMEDIATE SOURCE:
 LIBRARY: GenBank
 CLONE: 1098617
 US-08-690-095-9

Query Match 19.2%; Score 196.5; DB 1; Length 179;
 Best Local Similarity 32.7%; Pred. No. 1.4e-13;
 Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;

QY 35 CSCVAITLGLTAVLSVLLYQWILCOGSR--YSTCASCSPCDRMKRYGNHCYFS 92
 DB 20 CLSLMA-FLGILKNSFKLSIEPAFTPGPIEIQKSDSCSCQKRWGRCNYFISSE 78
 QY 93 EKDNSSLEFCLARDSHLIVTDNOMSLQVFLSEAFWIGL---RNSGWRMDGSP 149
 DB 79 QRTWNSRHLCASOKSLLQNTDELDFMS--SSQFTWIGLSTSEHTAWLWENGSL 136
 QY 150 NPSRISSNSF---VOTGAIKNG--LOASSCEVPLHGCK 186
 DB 137 --SQYLFPSFEFTFKNCIAYNPNGNALDESCEDKNRYICKQ 176

RESULT 8

US-08-650-578-2

Sequence 2, Application US/08650578

Patent No. 5811284

GENERAL INFORMATION:
 APPLICANT: Chang, Chiwen
 APPLICANT: Aramburu Beltran, Jose
 APPLICANT: Lopez-Botet, Miguel
 APPLICANT: Phillips Jr., Joseph H.
 APPLICANT: Lanier, Lewis L.
 TITLE OF INVENTION: Purified Mammalian NK Antigens and
 TITLE OF INVENTION: Related Reagents
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DNAX Research Institute
 STREET: 901 California Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94304-1104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/650,578
 FILING DATE:
 CLASSIFICATION: 514
 PRIOR APPLICATION NUMBER:
 APPLICATION NUMBER: US 08/175,339
 FILING DATE: 29-DEC-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Ching, Edwin P.
 REGISTRATION NUMBER: 34,090
 REFERENCE/DOCKET NUMBER: DX0391
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-852-9196
 TELEFAX: 415-496-1200
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 179 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-650-578-2

Query Match 19.2%; Score 196.5; DB 2; Length 179;

Best Local Similarity 32.7%; Pred. No. 1.4e-13;

Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;

QY 35 CGLVAITLGLTAVLVSVLYOMILCOGSN--YSTCASCSPCDRMMKYGHCYFVSVE 92

DB 20 CLSLMA-TLGLILKNSFTKLSTIEPAFTPGPIELQKSDCCSCQCKWVGRCNCYFISSE 78

QY 93 EKDNWSLEFLCARDSHLVITDNOEMSLLOVFLSEAFWCIGL---RNNSGWRWEDGSP 149

DB 79 OKTWNESRHLCAOSKSSILLOLQNTDELDFMS--SSQCFYWGIGLSYSEHTAMLMENGSA 136

QY 150 NFSRISNSF---VOTGAIKNG-LQASSCEVPLHGVCCK 186

DB 137 --SOYLFPSEFTFNTKNCIAYNPNGNALDESCEDKRNRYICKQ 176

RESULT 9

US-08-688-342-3

Sequence 3, Application US/08688342

Patent No. 5871964

GENERAL INFORMATION:

APPLICANT: Au-Young, Janice

APPLICANT: Cocks, Benjamin G.

APPLICANT: Goll, Surya K.

APPLICANT: Hillman, Jennifer L.

TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: US

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTED Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/688,342

FILING DATE: Filed Herewith

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0095-1 CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555

TELEFAX: 415-845-4166

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 179 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

IMMEDIATE SOURCE:

LIBRARY: Genbank

CLONE: 1098616

US-08-688-342-3

Query Match 19.2%; Score 196.5; DB 2; Length 179;

Best Local Similarity 32.7%; Pred. No. 1.4e-13;

Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;

QY 35 CGLVAITLGLTAVLVSVLYOMILCOGSN--YSTCASCSPCDRMMKYGHCYFVSVE 92

DB 20 CLSLMA-TLGLILKNSFTKLSTIEPAFTPGPIELQKSDCCSCQCKWVGRCNCYFISSE 78

QY 93 EKDNWSLEFLCARDSHLVITDNOEMSLLOVFLSEAFWCIGL---RNNSGWRWEDGSP 149

DB 79 OKTWNESRHLCAOSKSSILLOLQNTDELDFMS--SSQCFYWGIGLSYSEHTAMLMENGSA 136

QY 150 NFSRISNSF---VOTGAIKNG-LQASSCEVPLHGVCCK 186

DB 137 --SOYLFPSEFTFNTKNCIAYNPNGNALDESCEDKRNRYICKQ 176

DB 20 CLSLMA-TLGLILKNSFTKLSTIEPAFTPGPIELQKSDCCSCQCKWVGRCNCYFISSE 78

QY 93 EKDNWSLEFLCARDSHLVITDNOEMSLLOVFLSEAFWCIGL---RNNSGWRWEDGSP 149

DB 79 OKTWNESRHLCAOSKSSILLOLQNTDELDFMS--SSQCFYWGIGLSYSEHTAMLMENGSA 136

QY 150 NFSRISNSF---VOTGAIKNG-LQASSCEVPLHGVCCK 186

DB 137 --SOYLFPSEFTFNTKNCIAYNPNGNALDESCEDKRNRYICKQ 176

RESULT 10

US-09-113-788-3

Sequence 3, Application US/09113788

Patent No. 5969104

GENERAL INFORMATION:

APPLICANT: Au-Young, Janice

APPLICANT: Cocks, Benjamin G.

APPLICANT: Goll, Surya K.

APPLICANT: Hillman, Jennifer L.

TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: US

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTED Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/113,788

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/688,342

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0095-1 CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555

TELEFAX: 415-845-4166

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 179 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

IMMEDIATE SOURCE:

LIBRARY: Genbank

CLONE: 1098616

US-09-113-788-3

Query Match 19.2%; Score 196.5; DB 2; Length 179;

Best Local Similarity 32.7%; Pred. No. 1.4e-13;

Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;

QY 35 CGLVAITLGLTAVLVSVLYOMILCOGSN--YSTCASCSPCDRMMKYGHCYFVSVE 92

DB 20 CLSLMA-TLGLILKNSFTKLSTIEPAFTPGPIELQKSDCCSCQCKWVGRCNCYFISSE 78

QY 93 EKDNWSLEFLCARDSHLVITDNOEMSLLOVFLSEAFWCIGL---RNNSGWRWEDGSP 149

DB 79 OKTWNESRHLCAOSKSSILLOLQNTDELDFMS--SSQCFYWGIGLSYSEHTAMLMENGSA 136

QY 150 NFSRISNSF---VOTGAIKNG-LQASSCEVPLHGVCCK 186

DB 137 --SOYLFPSEFTFNTKNCIAYNPNGNALDESCEDKRNRYICKQ 176

Db 137 --SOYLEPSEFETNTKNCIAIYNPNGNALDESCEDKNRYICKQ 176

RESULT 11

US-09-113-789-9

Sequence 9, Application US/09113789

Patent No. 6034219

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

APPLICANT: Au-Young, Janice

APPLICANT: Gell, Surya K.

TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: U.S.

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

OPERATING SYSTEM: IBM Compatible

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/113,789

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/690,095

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0110 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555

TELEFAX: 415-845-4166

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 179 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

IMMEDIATE SOURCE:

LIBRARY: GenBank

CLONE: 1098617

US-09-113-789-9

Query Match

Best Local Similarity 32.7%; Pred No. 14e-13;

Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;

Db 35

35 CSCLVAITGLTAVLAVLTYLQWILCOGSN--YSTCASCPCSPDRMKNYGNHCYFYSVE 92

20 CISTWA-TIGILLKNSFTLSTEPATPPNIELOKDSOCCSQEKWVGRCYCFISSR 78

93 EKDWSSLEFCIARDSHLIVITDNDMSILQYFLSEAFWCIGL--RNSGWRWEDGSP 149

79 OKTWNSRHLICASQKSSLLQLONTDELDFMS--SSOOFYWGIGSYSEHTAWLWENGSA 136

150 NNSRISSNSF---VOTGAINKNG-LQASSCEVPLHGYCK 186

137 --SOYLEPSEFETNTKNCIAIYNPNGNALDESCEDKNRYICKQ 176

Db 137

137

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137

APPLICANT: Ziegler, Steven F.

APPLICANT: Hjerild, Kathryn A.

TITLE OF INVENTION: Activation Antigen CD69

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/10418

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Seese, Kathryn A.

REGISTRATION NUMBER: 32,172

REFERENCE/DOCKET NUMBER: 2610-WO

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 587-0430

TELEFAX: (206) 233-0644

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 199 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US93-10418-4

Query Match

Best Local Similarity 27.2%; Pred. No. 1.6e-13;

Matches 52; Conservative 27; Mismatches 79; Indels 33; Gaps 7;

Db 17

17 QANDYGPQ--QKSSSSKPCSCIAITLGLTAVLAVLTYLQWILCOGSNYSSTCASC 73

18 RCKDHGTSIHFEKHHEG---SIQVSIWAVLIVLITSLIALALANVGYK---NCP 69

74 -----SCPDMMKKNYGNHCYFYSVEKDNMSLECLARDSHLIVITDNOEM 119

70 GYKLESSDHHVATCKNEMISTYKTCYFESTTKSMALQKSCSEDAATLAVIDSKDM 129

120 SILQVFLSEAFWCIGLNR--NSGWRWEDGSPLN--FSRISSNSFVOTGAINKNGLOASS 175

130 TFLKRTSGLEHWIGLAKNEANQTKKANGKEFNWNLGSG---RCVSVNHKNVTAYD 185

176 CEVPLHGYCK 186

186 CEANFHWVCSK 196

Db 186

186

186

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APPLICANT: Ziegler, Steven F.

APPLICANT: Hjerild, Kathryn A.

TITLE OF INVENTION: Activation Antigen CD69

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/10418

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Seese, Kathryn A.

REGISTRATION NUMBER: 32,172

REFERENCE/DOCKET NUMBER: 2610-WO

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 587-0430

TELEFAX: (206) 233-0644

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 199 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US93-10418-4

Query Match

Best Local Similarity 27.2%; Pred. No. 1.6e-13;

Matches 52; Conservative 27; Mismatches 79; Indels 33; Gaps 7;

Db 17

17 QANDYGPQ--QKSSSSKPCSCIAITLGLTAVLAVLTYLQWILCOGSNYSSTCASC 73

18 RCKDHGTSIHFEKHHEG---SIQVSIWAVLIVLITSLIALALANVGYK---NCP 69

74 -----SCPDMMKKNYGNHCYFYSVEKDNMSLECLARDSHLIVITDNOEM 119

70 GYKLESSDHHVATCKNEMISTYKTCYFESTTKSMALQKSCSEDAATLAVIDSKDM 129

120 SILQVFLSEAFWCIGLNR--NSGWRWEDGSPLN--FSRISSNSFVOTGAINKNGLOASS 175

130 TFLKRTSGLEHWIGLAKNEANQTKKANGKEFNWNLGSG---RCVSVNHKNVTAYD 185

176 CEVPLHGYCK 186

186 CEANFHWVCSK 196

Db 186

186

186

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186

FILING DATE: 31-JUL-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Goldberg, Jules E
 REGISTRATION NUMBER: 24408
 REFERENCE/DOCKET NUMBER: JG-YY-4363PCT/D
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212 986-4090
 TELEFAX: 212 818-9479
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 270 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-352-302-2

Query Match 18.9%; Score 193; DB 4; Length 270;
 Best Local Similarity 30.6%; Pred. No. 5.7e-13;
 Matches 44; Conservative 25; Mismatches 53; Indels 22; Gaps 5;

QY	57	QWILQGSNYSSTCASCPCPDPMKYNHGYFVSEKEDMNSLEFCLARDSHLVTDN	116
DB	127	QEVLEKAAVNS-----GPCPDMLWHEENCYQFSSGPFNWEKSEQENCLSIDAHLTKINST	181
QY	117	QEMSLQVFLSEAF--CWIGL--RNSGWRWEDGSPLN-----FSRISSNSFVQT	162
DB	182	DELEPIQOMIAHSSPFWGLSMRKPNYSWLMWEDGTPLPHLFRIQGAVSRYMPGSG--T	238
QY	163	CGAINKNGLOASSCEVPLHGVCCK	186
DB	239	CAYIORGTIVFAENCILITAFSTICOK	262

Search completed: September 9, 2002, 15:00:04
 Job time: 1123 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 9, 2002, 14:39:55 : Search time 30.06 seconds
(without alignments)
698.368 Million cell updates/sec

Title: US-09-811-367b-1
Perfect score: 1023
Sequence: 1 MTDVSVIXSMLELPATQAQN.....GLQASCEPPLHGVCCKVRL 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A.Geneseq_032802.*

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22:	/SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1023	100.0	189	20	AAW88265
2	1023	100.0	189	22	AAE11759
3	789	77.1	843	22	ABG05451
4	548.5	53.6	188	22	AAE11760
5	525.5	51.4	188	16	AAK77032
6	525.5	51.4	188	20	AAW88277
7	525.5	51.4	188	22	AAE11761
8	431	42.1	99	20	AAW88267
9	370.5	36.2	114	16	AAK77472
10	306.5	30.0	70	20	AAW88266
11	226	22.1	198	22	AAW88815

12	226	22.1	198	22	AAU19820
13	226	22.1	203	22	AAU19659
14	217	21.2	35	22	ABR27967
15	217	21.2	35	22	ABR33139
16	217	21.2	35	22	ABR18604
17	217	21.2	35	22	AAW53935
18	217	21.2	35	22	AAW66323
19	217	21.2	35	22	AAW14192
20	217	21.2	35	22	AAW26602
21	217	21.2	35	22	AAW01928
22	216.5	21.2	182	22	AAU19660
23	201	19.6	225	16	AAE5189
24	197	19.3	218	22	AAE68584
25	196.5	19.2	179	19	AAW64791
26	196.5	19.2	179	19	AAW40232
27	196.5	19.2	199	15	AAE54660
28	196.5	19.2	199	15	AAE55595
29	195.5	19.1	278	22	AAE85871
30	193	18.9	257	20	AAW85594
31	193	18.9	270	17	AAE99586
32	193	18.9	270	20	AAE24152
33	193	18.9	270	22	AAE85870
34	193	18.9	273	17	AAE95867
35	193	18.9	243	10	AAE24153
36	191	18.7	233	13	AAE28118
37	190	18.6	233	19	AAW40231
38	190	18.6	265	22	AAU19657
39	187.5	18.3	238	22	AAE72948
40	186	18.2	325	21	AAE94345
41	185.5	18.1	316	20	AAW88125
42	184	18.0	215	19	AAW40220
43	183	17.9	215	13	AAE28121
44	182	17.8	231	19	AAW40219
45	181	17.7	273	17	AAE9368

ALIGNMENTS

RESULT	1	
ID	AAW88265	standard; Protein; 189 AA.
XX	AAW88265;	
XX	29-MAR-1999	(first entry)
XX	Human mast cell function-associated antigen (MAFA).	
XX	Mast cell function-associated antigen; MAFA; splice variant; human;	
KW	Inflammation; allergy; asthma; rheumatoid arthritis; tumour;	
KW	therapy.	
XX		
OS	Homo sapiens.	
XX		
PH	Key	Location/Qualifiers
FT	Modified-site	65..67
FT	Modified-site	/note="Asn is N-glycosylated"
FT	Modified-site	97..99
FT	Modified-site	/note="Asn is N-glycosylated"
FT	Modified-site	137..139
FT	Modified-site	/note="Asn is N-glycosylated"
FT	Modified-site	150..152
FT	Modified-site	/note="Asn is N-glycosylated"
FT	Peptide	7..10
FT		/note="ITIM motif"
XX	WO9854209-A2.	
XX	03-DEC-1998.	
PD		
XX		
PF	29-MAY-1998;	98MO-GB01572.
XX		


```
XX 11-OCT-2001.
PD
XX 30-MAR-2001; 2001WO-US08631.
XX
XX 31-MAR-2000; 2000US-0540217.
XX
XX 23-AUG-2000; 2000US-0649167.
XX
XX (HSE-) HSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YF;
XX
XX WPI: 2001-639332/73.
XX
XX N-PSDB: AAS69638.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity
XX
XX Claim 20; SEQ ID No 35810; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. AAG00010-ABG30377 represent novel human
XX CC Note: The sequence data for this patent did not appear in the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 843 AA:
SQ
Query Match 77.1%; Score 789; DB 22; Length 843;
Best Local Similarity 89.9%; Pred. No. 3.1e-73;
Matches 143; Conservative 8; Mismatches 8; Indels 0; Gaps 0;
OY 11 ELPTAQAONDYGPQOKSSSKPSCSCLVAITGLTAVLLSVLYQWILCOGSNYSTCA 70
Db 665 elptatqagndygpqgksssrpscsclvaialglltavllsvlyqwlccgsnystca 724
OY 71 SCPPSCDPRMKTGNHCYYSVEEKDNSSLEFCLARDSHLLVTTDQEMSLLOVFLSEAF 130
Db 725 scppscdprmktygnhcyysveekdnsslefcldardshllvltldqemsllygfllseaf 784
OY 131 CWIGLRNNSGWRWEDGSPINFSRISNSFVOTGCAINKN 169
Db 785 cwiglrmnsgrwewdgsplnfrtrntnglltrkxlnkn 823
RESULT 4
AAE11760 standard; Protein; 188 AA.
XX
XX AAE11760;
XX
XX 18-DEC-2001 (first entry)
XX
XX Mouse mast cell function associated antigen (MAFA) protein.
DE
```

```
XX
XX Mouse; pharmaceutical composition; mast cell function associated antigen;
XX MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;
XX immunosuppressive; cytostatic.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
XX Domain 64..188
XX /note="Extracellular domain"
XX
XX WO200170805-A2.
XX
XX 27-SEP-2001.
XX
XX 16-MAR-2001; 2001WO-US08596.
XX
XX 17-MAR-2000; 2000US-190716P.
XX
XX (GEMINI-) GEMINI SCI INC.
XX
XX Takahashi N, Miyayama T;
XX
XX WPI: 2001-611482/70.
XX
XX N-PSDB: AAD18735.
XX
XX Pharmaceutical composition for treating tumor by stimulating cytotoxic
XX activity of natural killer cell or T-cell, comprises an agent that
XX binds to mast cell function-associated antigen ligand on target cell
XX
XX Example 1; Page 19; 49pp; English.
XX
XX The present invention relates to a pharmaceutical composition comprising
XX an agent which specifically binds to a mast cell function associated
XX antigen (MAFA) ligand on a target cell, and prevents or inhibits natural
XX killer (NK)- or T-cell-expressed cell surface MAFA from binding to MAFA
XX ligand and a pharmaceutically acceptable excipient. The invention is
XX useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA
XX binding to a ligand on a target cell, by contacting the pharmaceutical
XX composition in vitro, ex vivo or in vivo by administering the composition
XX to the subject, to NK or T-cell or the target cell e.g. tumour cell, in
XX an amount sufficient to inhibit cell surface MAFA binding to the ligand
XX on the target cell. The agent or the composition is useful for treating a
XX tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic
XX T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible
XX tumour cell. The invention is also useful for inhibiting an activity of
XX NK cell or a T-cell. The present sequence is mouse MAFA protein.
XX
XX Sequence 188 AA:
SQ
Query Match 53.6%; Score 548.5; DB 22; Length 188;
Best Local Similarity 55.6%; Pred. No. 4.8e-49;
Matches 104; Conservative 26; Mismatches 56; Indels 1; Gaps 1;
OY 1 WTDSVITSMELPPTAQAONDYGPQOKSSSKPSCSCLVAITGLTAVLLSVLYQWIL 60
Db 1 mtdsvitstmelppptaqaondygpqgksssrpscsclvaialglltavllsvlyqwl 60
OY 61 COGSNYSTCA SCPPSCDPRMKTGNHCYYSVEEKDNSSLEFCLARDSHLLVTTDQEMS 120
Db 61 cogsnystcasppscdprmktygnhcyysveekdnsslefcldardshllvltldqem 120
OY 121 LLOVFLSEAFQWIGLRNNSGWRWEDGSPINFSRISNSFVOTGCAINKNGLOASCEVPL 180
Db 121 llfeylsgddfywlglnldgwrwegpalst-rltlnslgrcgaibhngqasceval 179
OY 181 HGVCCKV 187
Db 180 gwlcckv 186
RESULT 5
```

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AAR77033
ID AAR77033 standard; Protein: 188 AA.
XX
AC AAR77033:
XX
DT 01-FEB-1996 (first entry)
XX
DE Mammalian mast cell function-associated antigen (MAFA).
XX
KM Mast cell function-associated antigen; MAFA; soluble; ligand;
KW identification; screening; inflammation; inflammatory; allergy;
XX allergic; prevention.
OS Rattus rattus.
XX
PN MO9527734-A1.
XX
PD 19-OCT-1995.
XX
PF 06-APR-1995; 95WO-US04258.
XX
PR 08-APR-1994; 94IL-0109257.
XX
PA (RYCU/) RYCUS A.
XX (YEDA ) YEDA RES & DEV CO LTD.
XX Gutmann MD, Pecht I, Tal M;
XX WPI: 1995-366356/47.
XX DR N-PSDB; AAT01471.
XX
PT Novel DNA encoding a mast cell function-associated antigen (MAFA) -
PT useful for screening for ligands of MAFA which are useful for
PT prevention of inflammatory and allergic reactions
XX
XX Claim 12: Page 37; 54pp; English.
PS
XX A soluble form of mast cell function-associated antigen (MAFA) can
XX be produced by recombinant techniques for use in the ligand-
XX screening assay. The ligands that are identified may be used alone
XX or in combination with the MAFA to prevent inflammatory and allergic
XX reactions.
XX
XX Sequence 188 AA:
SQ
Query Match 51.4%; Score 525.5; DB 16; Length 188;
Best Local Similarity 53.5%; Pred. No. 1.2e-46;
Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;
1
1 MTDSEVYSMLELPTATQANDYGPOQSSSSKPSCLVATITGLITAVLSVLLYQWL 60
1 madnslystlelpaaprvgddsrwkvkavlhrpcvsylmvalglltvlmslllygrtl 60
DB
QY 61 CGGSNYSSTCASPSPCDPRMKMGKGNHCYFVSVEKDMNSLEPCLRDHLVITTDQEMS 120
DB 61 ccgskgfmcsqscrcpnlmtmngshoyfsmekrdmslskfcadkgslltlfpdngvvn 120
DB 1 LLOVFLSEAFQWIGLRNNSGWRMEDGSPINFSRISNSFVOTGAINKNGLOASSCEVPL 180
DB 1 lfgeyvgedfywlgtrldidgrwredgpalsls-llsnsvvgkcgltlhrcglnhasceval 179
QY 181 HGVCCKV 187
DB 180 gwicekv 186
RESULT 6
AAM88277
ID AAM88277 standard; Protein: 188 AA.
XX
AC AAM88277:
XX

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DT 29-MAR-1999 (first entry)
XX
XX Rat mast cell function-associated antigen (MAFA).
DE
XX Mast cell function-associated antigen; MAFA; splice variant; rat;
KW inflammation; allergy; asthma; rheumatoid arthritis; tumour;
XX therapy.
XX
OS Rattus sp.
XX
FH Key Location/Qualifiers
FH Modified-site 82..84
FT /note= "Asn is N-glycosylated"
FT Modified-site 97..99
FT /note= "Asn is N-glycosylated"
XX
PN MO9854209-A2.
XX
PD 03-DEC-1998.
XX
PF 29-MAY-1998; 98WO-GB01572.
XX
PR 31-MAY-1997; 97GB-0011148.
XX
PA (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX
PI Hewitt EL, Lamers MBAC, Lamont A, Williams DH;
XX
XX WPI: 1999-059806/05.
XX DR N-PSDB; AAV84222.
XX
XX New polypeptide having a sequence corresponding to human mast cell
PT function-associated antigen - useful in forming and manufacturing
PT pharmaceutical compositions in the treatment of inflammatory and
PT allergic diseases, and tumour growth
XX
XX Disclosure; Fig 4: 44pp; English.
PS
XX This is the amino acid sequence of rat mast cell function-associated
XX antigen (MAFA), a type II membrane glycoprotein found on mast cells
XX and basophils. The invention relates to cloning of the human MAFA
XX molecule (see AAM88265) and to the discovery of splice variants (see
XX AAM88266-67) of human MAFA that are not found in rat. Polypeptides
XX and synthetic peptides (see AAM88258-64) based on human MAFA and
XX human truncated MAFA, and polynucleotides encoding them, can be
XX used in methods for the treatment of inflammatory and allergic
XX diseases (e.g. rheumatoid arthritis and asthma), and tumour growth.
XX
XX Sequence 188 AA:
SQ
Query Match 51.4%; Score 525.5; DB 20; Length 188;
Best Local Similarity 53.5%; Pred. No. 1.2e-46;
Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;
1
1 MTDSEVYSMLELPTATQANDYGPOQSSSSKPSCLVATITGLITAVLSVLLYQWL 60
1 madnslystlelpaaprvgddsrwkvkavlhrpcvsylmvalglltvlmslllygrtl 60
DB
QY 61 CGGSNYSSTCASPSPCDPRMKMGKGNHCYFVSVEKDMNSLEPCLRDHLVITTDQEMS 120
DB 61 ccgskgfmcsqscrcpnlmtmngshoyfsmekrdmslskfcadkgslltlfpdngvvn 120
DB 1 LLOVFLSEAFQWIGLRNNSGWRMEDGSPINFSRISNSFVOTGAINKNGLOASSCEVPL 180
DB 1 lfgeyvgedfywlgtrldidgrwredgpalsls-llsnsvvgkcgltlhrcglnhasceval 179
QY 181 HGVCCKV 187
DB 180 gwicekv 186
RESULT 7

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	Query Match	51.4%;	Score 525.5;	DB 22;	Length 188;	
	Best Local Similarity	53.5%;	Pred. No. 1.2e-46;			
	Matches 100;	Conservative	29;	Mismatches 57;	Indels 1;	Gaps 1.
OY	1	MTDSVIYSMLPLPTAQNNDYGPOOKSSSKSPSCSLVATITLGLTAVLLSVLYQWIL	60			
		: : : : : : : : : : : : : : : : : : :				
Dd	1	madsuvsitltpaaaprvqddstmkvkaivilnpccvsiymwvalgiltylmwllilyqrfl	60			
OY	61	CQGSNYSYCASCPCSPCDWMKMGKNICYFYFSEVEEKMNSSLLEFLCLARDSHLTITPNOEMS	120			
		: : : : : : : : : : : : : : : : : : :				
Dd	61	cqgsqfmcscgscrpcrlwmrnngshncyifsmekridwnsslkfcadkysnlltfpdngyn	120			
OY	121	LLOVYLSEAFWCIGIRNNNSGWRMEDESGPLNEFRISNSSPVQCGLINKKLGLOASSCEVL	180			
		: : : : : : : : : : : : : : : : : : :				
Dd	121	lfgevyvedfyilgrldldidgwmedpalstls-ltsnsyvdgcgtchrcgltnassceval	179			
OY	181	HGVCKV 187				
		: : :				

Query Match	42.1%	Score 431	DB 20	Length 99	
Best Local Similarity	50.3%	Pred. No. 3.5e-37			
Matches 95	Conservative 1	Mismatches 3	Indels 90	Gaps 1	
QY	1	MTDSVYISMELPPTAQANDYGPQOKSSSKPSCSCIAVATLGLLTVALLSVLLYQWIL	60		
Db	1	mtdsyismelplptatqandypbqkssssrpsccscivalalglitvllsvlllyqwl	60		
QY	61	CGSGSYSTCASCPCSPDRMKRTGNHCYFYVEEKDMWNSLEFCLAROSHLLVITDQEMS	120		
Db	61	cqg-----	63		
QY	121	LLQYFLSAPFCWIGLRNNSGRWEDGSPLNRSRTSSNFVOTCGAIKNGLOASCEVPL	180		
Db	64	-----tsnsvqgcaltknnglqascevpil	90		
QY	181	HGYCKRYRL	189		

KM	cytostatic; gene therapy; vaccine; metastasis.	
XX	Homo sapiens.	
OS		
XX	MO200157182-A2.	
PN		
XX		
PD	09-AUG-2001.	
XX		
PF	17-JAN-2001; 2001MO-US01354.	
XX		
PR	31-JAN-2000; 2000US-0179065.	
PR	04-FEB-2000; 2000US-0180628.	
PR	24-FEB-2000; 2000US-0184664.	
PR	02-MAR-2000; 2000US-0186350.	
PR	16-MAR-2000; 2000US-0189874.	
PR	17-MAR-2000; 2000US-0190076.	
PR	18-APR-2000; 2000US-0198123.	
PR	19-MAY-2000; 2000US-0205515.	
PR	07-JUN-2000; 2000US-0209467.	
PR	28-JUN-2000; 2000US-0214886.	
PR	30-JUN-2000; 2000US-0215135.	
PR	07-JUL-2000; 2000US-0216647.	
PR	11-JUL-2000; 2000US-0217487.	
PR	11-JUL-2000; 2000US-0217496.	
PR	14-JUL-2000; 2000US-0218290.	
PR	26-JUL-2000; 2000US-0220963.	
PR	26-JUL-2000; 2000US-0220964.	
PR	14-AUG-2000; 2000US-0224519.	
PR	14-AUG-2000; 2000US-0225213.	
PR	14-AUG-2000; 2000US-0225214.	
PR	14-AUG-2000; 2000US-0225266.	
PR	14-AUG-2000; 2000US-0225267.	
PR	14-AUG-2000; 2000US-0225268.	
PR	14-AUG-2000; 2000US-0225270.	
PR	14-AUG-2000; 2000US-0225447.	
PR	14-AUG-2000; 2000US-0225757.	
PR	14-AUG-2000; 2000US-0225758.	
PR	14-AUG-2000; 2000US-0225759.	
PR	18-AUG-2000; 2000US-0226279.	
PR	22-AUG-2000; 2000US-0226681.	
PR	22-AUG-2000; 2000US-0226688.	
PR	22-AUG-2000; 2000US-0227182.	
PR	23-AUG-2000; 2000US-0227009.	
PR	30-AUG-2000; 2000US-0228924.	
PR	01-SEP-2000; 2000US-0229287.	
PR	01-SEP-2000; 2000US-0229343.	
PR	01-SEP-2000; 2000US-0229344.	
PR	01-SEP-2000; 2000US-0229345.	
PR	05-SEP-2000; 2000US-0229509.	
PR	05-SEP-2000; 2000US-0229513.	
PR	06-SEP-2000; 2000US-0230437.	
PR	06-SEP-2000; 2000US-0230438.	
PR	08-SEP-2000; 2000US-0231242.	
PR	08-SEP-2000; 2000US-0231243.	
PR	08-SEP-2000; 2000US-0231244.	
PR	08-SEP-2000; 2000US-0231413.	
PR	08-SEP-2000; 2000US-0231414.	
PR	08-SEP-2000; 2000US-0232080.	
PR	08-SEP-2000; 2000US-0232081.	
PR	12-SEP-2000; 2000US-0231968.	
PR	14-SEP-2000; 2000US-0232397.	
PR	14-SEP-2000; 2000US-0232398.	
PR	14-SEP-2000; 2000US-0232399.	
PR	14-SEP-2000; 2000US-0232400.	
PR	14-SEP-2000; 2000US-0232401.	
PR	14-SEP-2000; 2000US-0233063.	
PR	14-SEP-2000; 2000US-0233064.	
PR	14-SEP-2000; 2000US-0233065.	
PR	21-SEP-2000; 2000US-0234223.	
PR	21-SEP-2000; 2000US-0234274.	
PR	25-SEP-2000; 2000US-0234997.	

PR	25-SEP-2000; 2000US-0234998.	
PR	26-SEP-2000; 2000US-0235484.	
PR	27-SEP-2000; 2000US-0235834.	
PR	27-SEP-2000; 2000US-0235836.	
PR	29-SEP-2000; 2000US-0236327.	
PR	29-SEP-2000; 2000US-0236367.	
PR	29-SEP-2000; 2000US-0236368.	
PR	29-SEP-2000; 2000US-0236369.	
PR	29-SEP-2000; 2000US-0236370.	
PR	02-OCT-2000; 2000US-0236802.	
PR	02-OCT-2000; 2000US-0237037.	
PR	02-OCT-2000; 2000US-0237038.	
PR	02-OCT-2000; 2000US-0237039.	
PR	02-OCT-2000; 2000US-0237040.	
PR	13-OCT-2000; 2000US-0239935.	
PR	13-OCT-2000; 2000US-0239937.	
PR	20-OCT-2000; 2000US-0240960.	
PR	20-OCT-2000; 2000US-0241221.	
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PR	20-OCT-2000; 2000US-0241808.	
PR	20-OCT-2000; 2000US-0241809.	
PR	20-OCT-2000; 2000US-0241826.	
PR	01-NOV-2000; 2000US-0244617.	
PR	08-NOV-2000; 2000US-0246474.	
PR	08-NOV-2000; 2000US-0246475.	
PR	08-NOV-2000; 2000US-0246476.	
PR	08-NOV-2000; 2000US-0246477.	
PR	08-NOV-2000; 2000US-0246478.	
PR	08-NOV-2000; 2000US-0246523.	
PR	08-NOV-2000; 2000US-0246524.	
PR	08-NOV-2000; 2000US-0246525.	
PR	08-NOV-2000; 2000US-0246526.	
PR	08-NOV-2000; 2000US-0246527.	
PR	08-NOV-2000; 2000US-0246528.	
PR	08-NOV-2000; 2000US-0246532.	
PR	08-NOV-2000; 2000US-0246609.	
PR	08-NOV-2000; 2000US-0246610.	
PR	08-NOV-2000; 2000US-0246611.	
PR	17-NOV-2000; 2000US-0246613.	
PR	17-NOV-2000; 2000US-0249207.	
PR	17-NOV-2000; 2000US-0249208.	
PR	17-NOV-2000; 2000US-0249209.	
PR	17-NOV-2000; 2000US-0249210.	
PR	17-NOV-2000; 2000US-0249211.	
PR	17-NOV-2000; 2000US-0249212.	
PR	17-NOV-2000; 2000US-0249213.	
PR	17-NOV-2000; 2000US-0249214.	
PR	17-NOV-2000; 2000US-0249215.	
PR	17-NOV-2000; 2000US-0249216.	
PR	17-NOV-2000; 2000US-0249217.	
PR	17-NOV-2000; 2000US-0249218.	
PR	17-NOV-2000; 2000US-0249244.	
PR	17-NOV-2000; 2000US-0249245.	
PR	17-NOV-2000; 2000US-0249264.	
PR	17-NOV-2000; 2000US-0249265.	
PR	17-NOV-2000; 2000US-0249297.	
PR	17-NOV-2000; 2000US-0249299.	
PR	01-DEC-2000; 2000US-0250160.	
PR	01-DEC-2000; 2000US-0250391.	
PR	05-DEC-2000; 2000US-0251030.	
PR	05-DEC-2000; 2000US-0251988.	
PR	05-DEC-2000; 2000US-0256779.	
PR	06-DEC-2000; 2000US-0251479.	
PR	08-DEC-2000; 2000US-0251856.	
PR	08-DEC-2000; 2000US-0251868.	
PR	08-DEC-2000; 2000US-0251869.	
PR	08-DEC-2000; 2000US-0251989.	
PR	11-DEC-2000; 2000US-0254097.	
PR	05-JAN-2001; 2001US-0259678.	

KW	Cerebroprotective; thrombolytic; antimicrobial; ophthalmic; cystostatic; antialzheimers; immune/autoimmune disease; HIV infection; anaemia;	PR	14-SEP-2000;	20000US-0233403
KW	human immunodeficiency virus; rheumatoid arthritis; multiple sclerosis;	PR	14-SEP-2000;	20000US-0233064
KW	Cancers; hyperproliferative disorder; breast neoplasm; melanoma;	PR	14-SEP-2000;	20000US-0233065
KW	Seary syndrome; Gaucher's disease; neurological diseases;	PR	21-SEP-2000;	20000US-0234223
KW	Alzheimer's disease; Parkinson's disease; cardiovascular disorder;	PR	21-SEP-2000;	20000US-0234274
KW	cardiac arrest; tachycardia; angina; infection; corneal infections;	PR	25-SEP-2000;	20000US-0234997
KW	wound healing; immunogen; gene therapy; antilense; food additive.	PR	25-SEP-2000;	20000US-0234998
XX		PR	26-SEP-2000;	20000US-0235484
XX	Homo sapiens.	PR	27-SEP-2000;	20000US-0235834
XX		PR	27-SEP-2000;	20000US-0235836
XX	WO200155368-A1.	PR	29-SEP-2000;	20000US-0236327
XX		PR	29-SEP-2000;	20000US-0236367
XX		PR	29-SEP-2000;	20000US-0236368
XX		PR	29-SEP-2000;	20000US-0236369
XX		PR	29-SEP-2000;	20000US-0236370
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XX		PR	02-OCT-2000;	20000US-0237040
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XX		PR	20-OCT-2000;	20000US-0241786
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XX		PR	20-OCT-2000;	20000US-0241808
XX		PR	20-OCT-2000;	20000US-0241809
XX		PR	20-OCT-2000;	20000US-0241826
XX		PR	01-NOV-2000;	20000US-0244617
XX		PR	08-NOV-2000;	20000US-0244674
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XX		PR	08-NOV-2000;	20000US-0244676
XX		PR	08-NOV-2000;	20000US-0244677
XX		PR	08-NOV-2000;	20000US-0244678
XX		PR	08-NOV-2000;	20000US-0246523
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XX		PR	08-NOV-2000;	20000US-0246525
XX		PR	08-NOV-2000;	20000US-0246526
XX		PR	08-NOV-2000;	20000US-0246527
XX		PR	08-NOV-2000;	20000US-0246532
XX		PR	08-NOV-2000;	20000US-0246609
XX		PR	08-NOV-2000;	20000US-0246610
XX		PR	08-NOV-2000;	20000US-0246611
XX		PR	08-NOV-2000;	20000US-0246613
XX		PR	17-NOV-2000;	20000US-0249207
XX		PR	17-NOV-2000;	20000US-0249209
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XX		PR	17-NOV-2000;	20000US-0249211
XX		PR	17-NOV-2000;	20000US-0249212
XX		PR	17-NOV-2000;	20000US-0249213
XX		PR	17-NOV-2000;	20000US-0249214
XX		PR	17-NOV-2000;	20000US-0249215
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XX		PR	17-NOV-2000;	20000US-0249217
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XX		PR	17-NOV-2000;	20000US-0249265
XX		PR	17-NOV-2000;	20000US-0249297
XX		PR	17-NOV-2000;	20000US-0249299
XX		PR	17-NOV-2000;	20000US-0249300
XX		PR	01-DEC-2000;	20000US-0250160
XX		PR	01-DEC-2000;	20000US-0250391
XX		PR	05-DEC-2000;	20000US-0251030
XX		PR	05-DEC-2000;	20000US-0251988
XX		PR	05-DEC-2000;	20000US-0256719
XX		PR	06-DEC-2000;	20000US-0256719

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OM protein - protein search, using sw model

Run on: September 9, 2002, 14:59:46 : Search time 27.34 Seconds
(Without alignments)
1195.905 Million cell updates/sec

Title: US-09-811-367B-1
Perfect score: 1023
Sequence: 1 MTDVITYSMLEPTAQAON.....GLQASSCEVPLHGVCAYRL 189

Scoring table:
BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp-archaea:*
2: sp-bacteria:*
3: sp-fungi:*
4: sp-human:*
5: sp-invertebrate:*
6: sp-mammal:*
7: sp-mhc:*
8: sp-organelle:*
9: sp-phage:*
10: sp-plant:*
11: sp-rodent:*
12: sp-virus:*
13: sp-vertebrate:*
14: sp-unclassified:*
15: sp-virus:*
16: sp-bacteriap:*
17: sp-archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1023	100.0	189	4	043198
2	1007	98.4	189	4	075613
3	994	97.2	195	4	096E93
4	548.5	53.6	188	11	088713
5	525.5	51.4	188	11	064335
6	226	22.1	231	4	09M252
7	225	22.0	181	4	09M251
8	219.5	21.5	275	11	09D403
9	210	20.5	227	11	09M132
10	210	20.5	231	11	054872
11	203	19.8	233	6	095M15
12	201.5	19.7	231	6	09M2K3
13	201	19.6	225	4	012918
14	199.5	19.5	180	6	09M2K8
15	199.5	19.5	231	6	09GK88
16	199.5	19.5	269	11	Q9D676

17	199	19.5	233	6	09MVM6	09MVM6 pan troglod
18	198.5	19.4	179	6	09M2K9	09M2K9 macaca mula
19	198.5	19.4	179	6	09GK91	09GK91 macaca mula
20	197	19.3	180	4	043773	043773 homo sapien
21	197	19.3	232	11	054709	054709 mus musculu
22	196.5	19.2	246	6	09M2K2	09M2K2 macaca mula
23	196	19.2	211	11	0912M5	0912M5 mus musculu
24	196	19.2	246	6	09M2K1	09M2K1 macaca mula
25	195.5	19.1	244	11	092202	092202 mus musculu
26	195.5	19.1	278	6	09XTA8	09XTA8 oryctolagus
27	194.5	19.0	178	11	0912W9	0912W9 mus musculu
28	194.5	19.0	179	6	09M241	09M241 pan troglod
29	193	18.9	257	13	090636	090636 gallus gall
30	193	18.9	270	6	P79391	P79391 bos taurus
31	192.5	18.8	208	11	0912W7	0912W7 mus musculu
32	192.5	18.8	244	11	09M031	09M031 mus musculu
33	192	18.8	236	6	095194	095194 macaca mula
34	191.5	18.7	230	11	054871	054871 rattus norv
35	191	18.7	148	6	09M2K7	09M2K7 macaca mula
36	190	18.6	199	6	095M01	095M01 bos taurus
37	190	18.6	227	11	061973	061973 mus musculu
38	189	18.5	226	6	09M239	09M239 pan troglod
39	188	18.4	124	4	09UB00	09UB00 homo sapien
40	188	18.4	148	4	043321	043321 homo sapien
41	188	18.4	231	4	09NR42	09NR42 homo sapien
42	187.5	18.3	231	6	09M2K5	09M2K5 macaca mula
43	187.5	18.3	238	11	0912X1	0912X1 mus musculu
44	187	18.3	179	11	035778	035778 rattus norv
45	187	18.3	231	6	09M238	09M238 pan troglod

ALIGNMENTS

RESULT 1
ID 043198 PRELIMINARY; PRT; 189 AA.
AC 043198:
DT 01-JUN-1998 (TEMBLrel. 06, Created)
DT 01-JUN-1998 (TEMBLrel. 06, Last sequence update)
DE 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE MAST CELL FUNCTION-ASSOCIATED ANTIGEN.
GN MAF.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-ENZYMIC DIGESTED LUNG;
RX MEDLINE=98438735; PubMed=9765598;
RA Lamers M.B., Lamont A.G., Williams D.H.;
RT "Human MAF has alternatively spliced variants";
RL Biochim. Biophys. Acta 1399:209-212(1998).
DR EMBL: AF034952; AAC34731.1; .
DR HSSP: P06734; IHLT.
DR InterPro: IPR001304; lectin_c.
DR Pfam: PF00059; lectin_c; 1.
DR SMART: SM00034; CLECT. 1.
DR PROSITE: PSS0041; C_TYPE_LLECTIN_2; 1.
SQ SEQUENCE 189 AA; 21079 MW; 15E042AD40B2BAF6 CRC64;

Query Match 100.0%; Score 1023; DB 4; Length 189;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDVITYSMLEPTAQAONDYGPQOKSSSKSPSCGLVATITGLTAVLLSVLYQWIL 60
DB 1 MTDVITYSMLEPTAQAONDYGPQOKSSSKSPSCGLVATITGLTAVLLSVLYQWIL 60
QY 61 CGGSNSTCASCPCSDRWKVIYGNHCYYSVEKDMNSSLFCLARDSHLLVTNDQMS 120


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Db 61 COGSNTSTCASCPCPDMMKTKGNHCYFVSVEKDMNSLFCCLARDSHLVTITNOEMS 120
QY 121 LLOVFLSEAFWCIGLRNNSGWRMEDGSPLNFSRISNSFVOTCGAINKNGLOASSCEVPL 180
Db 121 LLOVFLSEAFWCIGLRNNSGWRMEDGSPLNFSRISNSFVOTCGAINKNGLOASSCEVPL 180
QY 181 HGVCCKKRL 189
Db 181 HGVCCKKRL 189

RESULT 2
075613 PRELIMINARY; PRT; 189 AA.
AC 075613;
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE ITIM-CONTAINING RECEPTOR MAFA-L.
GN MAFA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Butcher S., Arney K.L., Cook G.P.;
RT "MAFA-L, an ITIM-containing receptor encoded by the human NK cell gene
RT complex and expressed by basophils and NK cells.";
RL Eur. J. Immunol. 28:0-0(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-99077194; PubMed-9862378;
RA Hanke T., Corral L., Vance R.E., Raulat D.H.;
RT "2F1 antigen, the mouse homolog of the rat '31', is a lectin-like type
RT II transmembrane receptor expressed by natural killer cells.";
RL Eur. J. Immunol. 28:4409-4417(1998).
DR EMBL; AF081675; AAC32200.1; -
DR HSSP; P06734; 1H1.
DR InterPro; IPR001304; lectin_C.
DR Pfam; PF00059; lectin_c.1.
DR SMART; SM00034; CLECT.1.
DR PROSITE; PS50041; C_Type_Lectin_2; 1
SQ SEQUENCE 189 AA; 21206 MW; FA9023F1523656A8 CRC64;

Query Match 98.4%; Score 1007; DB 4; Length 189;
Best Local Similarity 98.4%; Pred. No. 4.3e-103;
Matches 186; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE SIMILAR TO KILLER CELL LECTIN-LIKE RECEPTOR SUBFAMILY G, MEMBER
DE 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BONE MARROW, AND ACUTE MYELOCYTIC LEUKEMIA;
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC012621; AAH12621.1; -
KW Receptor; Lectin.
SQ SEQUENCE 195 AA; 21831 MW; 178E98E08EBC473 CRC64;

Query Match 97.2%; Score 994; DB 4; Length 195;
Best Local Similarity 98.4%; Pred. No. 1.2e-101;
Matches 183; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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RL Immunogenetics 52:206-211(2001).
DR EMBL: AF097357; RAD03718.1; -
DR EMBL: AJ010751; CA00342.1; -
DR EMBL: AF317727; AAK40082.1; -
DR MGD: MGI:1355294; K1rg1.
DR InterPro: IPR001304; Lectin_c.
DR Pfam: PF00059; lectin_c; 1.
DR SMART: SM00034; lectin_c; 1.
DR PROSITE: PS50041; C_TYPE_LLECTIN_2; 1.
DR Receptor: Lectin.
KW SEQUENCE 188 AA; 21396 MW; 876336802EA134F1 CRC64;

Query Match 53.6%; Score 548.5; DB 11; Length 188;
Best Local Similarity 55.6%; Pred. No. 1.6e-52;
Matches 104; Conservative 26; Mismatches 56; Indels 1; Gaps 1;

QY 1 MDSVYISMLELPTATQANDYGPQKSSSSKPSCLVAITGLTAVLLSVLYQWIL 60
DB 1 MADSSISYSLLELPEAPQVODESRMKLKAVALHRPHLSRPAVALGLTLVILMSLTMQRTL 60
QY 61 CGSNSTSCASCSPCPDRMKKYGHCYFFSVYEEDKWNSSLEFCLARDSHLVITDQEMS 120
DB 61 CGSSKSTSCSPCPDILMTKNGSHCYFFSMERKWNSSLEKFCADKSHLLTFPDQGVK 120
QY 121 LQVLESEAFQWIGLRNNSGMRWEDSGPLNFSRISNSFVOTGAINKNGLOASSCEVPL 180
DB 121 LFEQYVEDPYWIGLRIDGWRNEDGPAISLILSNVYQKCGTIRRCGLHASSCEVAL 179
QY 181 HGVCCKV 187
DB 180 OWICEKV 186

RESULT 5

ID 064335 PRELIMINARY; PRT; 188 AA.

AC 064335;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE MAFR PROTEIN.
GN MAFR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE DAWLEY; TISSUE=TESTIS;
RA Bocek Jr P., Gutmann M.D., Pecht I.;
RL Submitted (APR-1996) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96016176; PubMed=7568140;
RA Gutmann M.D., Tal M., Pecht I.;
RT "A secretion inhibitory signal transduction molecule on mast cells is
another C-type lectin."
RL Proc. Natl. Acad. Sci. U.S.A. 92:9397-9401(1995).
DR EMBL: X97191; CA65829.1; -
DR EMBL: X97192; CA65829.1; JOINED.
DR EMBL: X97193; CA65829.1; JOINED.
DR EMBL: X97194; CA65829.1; JOINED.
DR EMBL: X97195; CA65829.1; JOINED.
DR EMBL: X79812; CA65829.1; -
DR InterPro: IPR001304; lectin_c.
DR Pfam: PF00059; lectin_c; 1.
DR SMART: SM00034; lectin_c; 1.
DR PROSITE: PS50041; C_TYPE_LLECTIN_2; 1.
SQ SEQUENCE 188 AA; 21356 MW; 2CC8032D4D020B15 CRC64;

Query Match 51.4%; Score 525.5; DB 11; Length 188;

Best Local Similarity 53.5%; Pred. No. 5.4e-50;
Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;

QY 1 MDSVYISMLELPTATQANDYGPQKSSSSKPSCLVAITGLTAVLLSVLYQWIL 60
DB 1 MADSSISYSLLELPEAPQVODESRMKLKAVALHRPHLSRPAVALGLTLVILMSLTMQRTL 60
QY 61 CGSNSTSCASCSPCPDRMKKYGHCYFFSVYEEDKWNSSLEFCLARDSHLVITDQEMS 120
DB 61 CGSSKSTSCSPCPDILMTKNGSHCYFFSMERKWNSSLEKFCADKSHLLTFPDQGVN 120
QY 121 LQVLESEAFQWIGLRNNSGMRWEDSGPLNFSRISNSFVOTGAINKNGLOASSCEVPL 180
DB 121 LFEQYVEDPYWIGLRIDGWRNEDGPAISLILSNVYQKCGTIRRCGLHASSCEVAL 179
QY 181 HGVCCKV 187
DB 180 OWICEKV 186

RESULT 6

ID 09NZS2 PRELIMINARY; PRT; 231 AA.

AC 09NZS2;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE LECTIN-LIKE RECEPTOR FL (ACTIVATING CORECEPTOR NKp80).
GN KLRF1 OR ML/KLRF1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20135860; PubMed=10671213;
RA Roda-Navarro P., Arce I., Renedo M., Montgomery K., Kucherlapati R.,
RA Fernandez-Puiz E.;
RT "Human KLRF1, a novel member of the killer cell lectin-like receptor
gene family: molecular characterization, genomic structure, physical
mapping to the NK gene complex and expression analysis."
RT Eur. J. Immunol. 30:568-576(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LIMPHOID;
RX MEDLINE=21150889; PubMed=11265639;
RA Vitale M., Falco M., Castriiconi R., Parolini S., Zambello R.,
RA Semenzato G., Blassoni R., Bottino C., Moretta L., Moretta A.;
RT "Identification of NKp80, a novel triggering molecule expressed by
human natural killer cells."
RL Eur. J. Immunol. 31:233-242(2001).
DR EMBL: AF175206; AAF37804.1; -
DR EMBL: AJ305370; CAC29425.1; -
DR InterPro: IPR001304; lectin_c.
DR Pfam: PF00059; lectin_c; 1.
DR SMART: SM00034; lectin_c; 1.
DR PROSITE: PS50041; C_TYPE_LLECTIN_2; 1.
KW Receptor.
SQ SEQUENCE 231 AA; 26562 MW; A2F7BE6D4341AFDE CRC64;

Query Match 22.1%; Score 226; DB 4; Length 231;

Best Local Similarity 31.2%; Pred. No. 7.4e-17;
Matches 58; Conservative 27; Mismatches 53; Indels 48; Gaps 8;

QY 44 GLTFVILSVLLY--QWIL--CGG-----SNSTSCASC 74
DB 49 GLTLFLISLILVLSQGVLLCKGKSCSNATQIEDTGDKLVNNGTRRNISNKLDCASRSA 108
QY 75 -----CPDRMKKYGHCYFFSVYEEDKWNSSLEFCLARDSHLVITDQEMSLQVLSFA 129
DB 109 DQTVLCQSEMLKYGKCYWFSNEMKMSMSDSYVYICLERKSHLLIHDOLEMAFIQKNLRDL 168

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QY 130 -FCWIGLRNNS---GWRWEDGSPLNFRSSNSFVQ-----TCGAINKNGLOASSCEVP 179
DB 169 NYWIGLNTSTSLKMTWTWVDGSPID-----SKIFFIKGPAKENSACAIFSKIFSETCSSV 224
QY 180 LHVGVCK 185
DB 225 FKWICQ 230

RESULT 7
ID 09NZS1 PRELIMINARY: PRT; 181 AA.
AC 09NZS1:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE LECTIN-LIKE RECEPTOR FL, SPLICED VARIANT 1 KLRF1-S1.
GN KLRF1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
ON NCBL_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20135860; PubMed=10671213;
RA Roda-Navarro P., Arce I., Renedo M., Montgomery K., Kucherlapati R.,
RA Fernandez-Ruiz E.,
RT "Human KLRF1, a novel member of the killer cell lectin-like receptor
RT gene family: molecular characterization, genomic structure, physical
RT mapping to the NK gene complex and expression analysis."
RL Eur. J. Immunol. 30:568-576(2000).
DR EMBL: AF175207; AAF37805.1; -
DR InterPro: IPR001304; lectin_c.
DR Pfam: PF00059; lectin_c; 1.
DR SMART: SM00034; CLECT. 1.
DR PROSITE: PS50041; C_TYPE_LECTIN_2; 1.
KM Receptor.
SQ SEQUENCE 181 AA; 21204 MW; 64642240CA1E551 CRC64;

Query Match 22.0%; Score 225; DB 4; Length 181;
Best Local Similarity 33.6%; Pred. No. 7.1e-17;
Matches 51; Conservative 26; Mismatches 45; Indels 30; Gaps 6;

QY 44 GILTAVALSVLYXOMILCGSNSTSCASPCSDRMKNGHCYYSVEKDMNSSLERC 103
DB 49 GILTLLISLILL--VLCO-----SEWLKYGCKYFSSNEKKSMSDSVYVC 92
QY 104 LARDSHLVTTTNOEMKSLQVFLSEA-FCWIGLRNNS--GWRWEDGSPLNFRSSNSF 159
DB 93 LERKSHLITIHOLEKAPLOKNIROLNYVIGLNTSTSLKMTWTWVDGSPID---SKIFF 148
QY 160 VQ-----TCGAINKNGLOASSCEVPLHGVCK 185
DB 149 IKGPAKENSACAIFSKIFSETCSSVFKWICQ 180

RESULT 8
ID 09D403 PRELIMINARY: PRT; 275 AA.
AC 09D403:
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE 4933425B16RIK PROTEIN.
GN 4933425B16RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBL_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=TESTIS;

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RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staudli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsi G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bona M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamaya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitlaker C., Wilming L.,
RA Wysshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK016908; BAB30491.1; -
DR HSSP: P23807; IIXX.
DR MGD: MGI:1918433; 4933425B16RIK.
DR InterPro: IPR001304; lectin_c.
DR Pfam: PF00059; lectin_c; 1.
DR SMART: SM00034; CLECT. 1.
DR PROSITE: PS50041; C_TYPE_LECTIN_2; 1.
SQ SEQUENCE 275 AA; 31360 MW; C9792BA25C9B5CC2 CRC64;

Query Match 21.5%; Score 219.5; DB 11; Length 275;
Best Local Similarity 31.6%; Pred. No. 4.7e-16;
Matches 60; Conservative 34; Mismatches 73; Indels 23; Gaps 9;

QY 16 TQANDYGPQOK--SSSSKPCSCGLVAITL--GILTAVAL-----LSVLLYXOMILCGSNYS 67
DB 79 SOLQKSIHPQODNLSELSNRSKSLFESLQSGISALHEQEQVATLCEFLIHASDH- 137
QY 68 TCASPCSDPDRMKNGHCYYSV--EEKDWNSSLERFLARDSHLVTTTNOEMSL--QV 124
DB 138 ---KCNPCFKTQWQYSGCYFSINEERKSWDSRDKDIDKNATLVKIDSTEERLLQSOL 194
QY 125 FLSEAFQWIGLR--NNSG--NRWEDG-----PLNFRSSNSFQTCGAINKNGLOASSC 176
DB 195 SLTFSEFVGLSWNSSGRNLMWEDGSPPTLLSDKELASFNGBECAYFERGNITVSRG 254
QY 177 EYPLHGVCK 186
DB 255 RAETPWICK 264

RESULT 9
ID 09WU32 PRELIMINARY: PRT; 227 AA.
AC 09WU32:
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE NATURAL KILLER CELL RECEPTOR NKGB2.
GN KLRC1 OR NKGB2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBL_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6;
RX MEDLINE=99190498; PubMed=10092077;
RX Lohwasser S., Hande P., Mager D.L., Takei F.;
RT "Cloning of murine NKGB2A, B and C: second family of C-type lectin
RT receptors on murine NK cells."
RL Eur. J. Immunol. 29:755-761(1999).

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DR EMBL: AF109784; AAD24970.1; -
 DR MGD: MG1:1336161; K1rc1.
 DR InterPro: IPR001304; lectin_c.
 DR Pfam: PF000059; lectin_c; 1.
 DR SMART: SM00034; CLECT; 1.
 DR PROSITE: PS50041; C_TYPE_LECTIN_2; 1.
 DR Receptor.
 SK SEQUENCE 227 AA; 25746 MW; 1651968539C28C86 CRC64;

Query Match 20.5%; Score 210; DB 11; Length 227;
 Best Local Similarity 27.1%; Pred. No. 4.2e-15;
 Matches 62; Conservative 33; Mismatches 78; Indels 56; Gaps 12;

QY 3 DSVYSLMELPTAQAQNDY-----GPG-----QKSSSRP-----SCSC 37
 DB 4 ERYVYA--ELKVAANSNQHKKPRGPNSSIVIOEIIYSPFSQNPQEPHWCRCNCPG 61
 QY 38 -----LVATLGLTAVLVLT-SVLLYQWILCOGSNY--STCASCPCSPDRMKYGNH 85
 DB 62 KGFPPSPPEKLIAGTGLICFLIVAVVITVATPYINTLSSAQPCPHCKEMISTYSHN 121
 QY 86 CYFVSVEEKDWNSSLEPCCLARDSHLVTIDNQESLLQVFLSEAFQWIG-LRNNSG--WR 142
 DB 122 CYFLGMRKSMNDSLVSCISKNCSLYIDSEEDFLOSL--SLISWTGLLRKGRGQPMV 179
 QY 143 WEGDSPINFRISNSFYQ-----TCGAINKNGLOASSCEVPLHGYCK 185
 DB 180 WKBDSS-----IFRPKIAELHDECNCAMMSAGSLTADNCTTLHPYLCK 222

RESULT 10

054872 ID 054872 PRELIMINARY; PRT; 231 AA.
 AC 054872;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE NATURAL KILLER CELL PROTEIN GROUP 2-A (FRAGMENT).
 GN NKG2A.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 OX [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=F344;
 RX MEDLINE=98180346; Pubmed=9521051;
 RA Berg S.F., Dissen E., Westgaard I.H., Fossum S.;
 RT "Molecular characterization of two genes in the rat homologous to
 human NKG2.";
 RL Eur. J. Immunol. 28:444-450(1998).
 DR EMBL: AF021350; AAC40050.1; -
 DR InterPro: IPR001304; lectin_c.
 DR Pfam: PF000059; lectin_c; 1.
 DR SMART: SM00034; CLECT; 1.
 DR PROSITE: PS50041; C_TYPE_LECTIN_2; 1.
 DR NON_TER 1
 FT 1
 SO SEQUENCE 231 AA; 26335 MW; FF2AB6D33EFZCE99 CRC64;

Query Match 20.5%; Score 210; DB 11; Length 231;
 Best Local Similarity 29.0%; Pred. No. 4.3e-15;
 Matches 54; Conservative 25; Mismatches 81; Indels 26; Gaps 5;

QY 24 PQQKSSSSKPCSC-----LVATLGLTAVLVLT-----YQWILCOGSNY 66
 DB 43 PSQQRICRCDCKHKGFPSPPEKLIAGTGLISFLIVAVVITVATPYETKQAINSS 102
 QY 67 ST-----CASCPCSPDRMKYGNHCYFVSVEEKDWNSSLEPCCLARDSHLVTIDNQESLL 122
 DB 103 MTRKYQARPCIRCDPMWISHNCTYISVERKSNMDSGLTSCISKNSLHIDSEEOAFL 162

QY 123 QVFLSEAFQWIGLRNNS---GWRMEDGSPINFRISNSFVOTCGAINKNGLOASSCEVP 179
 DB 163 QSF--SLVSWGCFRFRKSNQPMWENGSTFRKRTIEMHDEYNCTIMSTSGLAENCTIL 220
 QY 180 LHGYCK 185
 DB 221 HPYVCK 226

RESULT 11

095MT5 ID 095MT5 PRELIMINARY; PRT; 233 AA.
 AC 095MT5;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE NKG2A.
 GN NKG2A.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pan.
 OC NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shum B.P., Flodin L.R., Muir D.G.;
 RT "CD94 and NKG2 Genes in Human and Common Chimpanzee."
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBS databases.
 DR EMBL: AF350005; AAK83792.1; -
 SO SEQUENCE 233 AA; 26231 MW; A993D9648000CC84 CRC64;

Query Match 19.8%; Score 203; DB 6; Length 233;
 Best Local Similarity 28.8%; Pred. No. 2.6e-14;
 Matches 57; Conservative 34; Mismatches 87; Indels 20; Gaps 7;

QY 5 VYVSLMELPTAQ--AONDYGPQKSSSKPSCCLVATLGLTAVLVLT-----SVLLYQW 58
 DB 38 IYVALNLQKASQDQENDKTYHCKDLPSAP--EKIIVGILGLICLIMASVTVIYVVS 95
 QY 59 ILCOGSNYST-----CASCPCSPDRMKYGNHCYFVSVEEKDWNSSLEPCCLARDSHLL 111
 DB 96 TLIQHNHNSLNTFRQKARHCHCEEWITVNSCYLIKERTWESLIACSKNSGILL 155
 QY 112 VITIDNQESLLQVFLSEAFQWIG-LRNNSGWRMEDGSPINFR--ISSNFVOTCGAINK 168
 DB 156 SIDNEEMKFLSIISPS--WIGVFRNSSHPWYTINGLAFRHEIKDSNAELNCAYLOY 213
 QY 169 NGLQASSCEVPLHGYCK 186
 DB 214 NGLKSAQCGSSITTYHCKR 231

RESULT 12

09MZK3 ID 09MZK3 PRELIMINARY; PRT; 231 AA.
 AC 09MZK3;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE NKG2-C.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OC NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20322487; Pubmed=10866118;
 RA Labonte M.L., Levy D.B., Letvin N.L.;
 RT "Characterization of rhesus monkey CD94/NKG2 family members and
 identification of novel transmembrane-deleted forms of NKG2-A, B, C,
 and D.";
 RL Immunogenetics 51:496-499(2000).

